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- ☐ 1. [20040234529](#). 22 Jan 04. 25 Nov 04. Helicobacter pylori adhesin binding group antigen. Boren, Thomas, et al. 424/164.1; 530/388.4 A61K039/40 C07K016/12.
- ☐ 2. [20020061545](#). 22 Jan 01. 23 May 02. Streptococcus pneumoniae antigens and vaccines. Choi, Gil H., et al. 435/7.34; 424/190.1 435/252.3 435/6 435/69.3 536/23.7 G01N033/569 C12Q001/68 C07H021/04 A61K039/02 C12N001/21.
- ☐ 3. [20020044949](#). 01 Apr 97. 18 Apr 02. 76 KDA HELICOBACTER POLYPEPTIDES AND CORRESPONDING POLYNUCLEOTIDE MOLECULES. KLEANTHOUS, HAROLD, et al. 424/235.1; A61K039/02.
- ☐ 4. [6887663](#). 22 Jan 01; 03 May 05. Streptococcus pneumoniae SP036 polynucleotides. Choi; Gil H., et al. 435/6; 435/252.3 435/254.11 435/257.2 435/320.1 435/325 435/471 435/69.1 435/69.7 435/70.1 536/23.7. C12Q00168 C12P02106 C12N01500 C07H02104.
- ☐ 5. [6709656](#). 10 Feb 99; 23 Mar 04. Helicobacter pylori adhesin binding group antigen. Boren; Thomas, et al. 424/190.1; 424/184.1 424/234.1 435/252.1 435/7.32 514/25 530/350. A61K039/02.
- ☐ 6. [6573082](#). 28 Mar 00; 03 Jun 03. Streptococcus pneumoniae antigens and vaccines. Choi; Gil H., et al. 435/252.3; 435/320.1 435/325 536/23.7. C12N001/20 C12N015/00 C12N005/00 C07H021/04.
- ☐ 7. [WO 200000614A](#). Novel Helicobacter pylori antigens useful for diagnostic and therapeutic purposes. DILTS, D A, et al. A61K038/16 A61K039/106 A61K039/40 C07K014/205 C07K014/34 C07K016/12 C12N001/21 C12N015/31 C12N015/62.

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	<i>DB=USPT; PLUR=YES; OP=AND</i>		
<input type="checkbox"/>	L1	blood near2 group near2 binding near2 protein	4
<input type="checkbox"/>	L2	antiadhesion or anti-adhesion or anti-adhesin or antiadhesin or antibab or antibaba or anti-bab or anti-bab-a or antibab\$3	963
<input type="checkbox"/>	L3	L2 and helicobacter	12
<input type="checkbox"/>	L4	L3 not l1	12
<input type="checkbox"/>	L5	L3 not l1	12
<input type="checkbox"/>	L6	antibab or antibaba or anti-bab or anti-bab-a or antibab\$3	6
<input type="checkbox"/>	L7	helicobacter near10 (adhesin or adherence or attachment or receptor)	56
<input type="checkbox"/>	L8	L7 and (blood or lewis)	51
<input type="checkbox"/>	L9	L7 same (blood or lewis)	17
<input type="checkbox"/>	L10	antihelicobacter	1
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<input type="checkbox"/>	L12	polyclonal same helicobacter same adhesin	0
<input type="checkbox"/>	L13	polyclonal same pylori same adhesin	3

END OF SEARCH HISTORY

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Set	Items	Description
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Executing TH43234556

>>>SET HILIGHT: use ON, OFF, or 1-5 characters

117113	HELICOBACT?
119190	PYLORI
271	PYLORIS
2373	PYLORIDIS
27	PYLORUM

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        124  HPYLORI
        22761  PORIN?
        60997  HOP
        291  HOPA
        154  HOPB
        55  HOPZ
        289617  HOPE
        4751  AU=LING
S1      306  (HELICOBACT? OR PYLORI OR PYLORIS OR PYLORIDIS OR PYLORUM
           OR HPYLORI) (100N) ((PORIN? OR HOP OR HOPA OR HOPB OR
           HOPZ OR HOPE) OR AU=LING)
? s s1/1997:2005
Processing
Processed 10 of 19 files ...
Processing
Completed processing all files
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        48288846  PY=1997 : PY=2005
        S2      253  S1/1997:2005
? s s1 not s2
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        253  S2
        S3      53  S1 NOT S2
?
? t s3/ti,kwic/all
>>>KWIC option is not available in file(s): 399

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Search for

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In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 20 AA

Date run: 2005-05-03 11:01:00 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,880,849 sequences; 604,459,357 total letters

UniProt Release 4.6 consists of: Swiss-Prot Release 46.6 of 26-Apr-2005: 180652 en
TrEMBL Release 29.6 of 26-Apr-2005: 1689375 entrie

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List of potentially matching sequences

Send selected sequences to


☐ Include query sequence



Db AC	Description	Score	E-value
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<input type="checkbox"/> tr Q8GNY0	_HELPHY BabB (Fragment) [babB] [Helicobacter pylori (Cam...	69	7e-12
<input type="checkbox"/> tr Q8GNX9	_HELPHY BabB (Fragment) [babB] [Helicobacter pylori (Cam...	69	7e-12
<input type="checkbox"/> tr Q8GNX7	_HELPHY BabB (Fragment) [babB] [Helicobacter pylori (Cam...	69	7e-12
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Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
( [Help](#)) (use ScanProsite for more details about PROSITE matches)

Profile hits 
Pfam hits 

Submission	Matches on query sequence	Mat
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Q5G5J6		
Q8GNY8		
Q8GNX9		
Q8GNX7		
Q8GNX5		
Q8GNX4		
Q8GNX3		
Q8GNX2		
Q8GNX1		
Q8GNW9		
Q8GNW8		
Q8GNW7		
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Q6T8D3		
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Q51811		
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Alignments

tr Q5G5J6 Adhesin-binding fucosylated histo-blood group (Fragment) 138
Q5G5J6_HELPY [babB] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 8 EDDGFYMSAGYQIGEEAQM 27

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Q8GNY0_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 6 EDDGFYMSAGYQIGEEAQM 25

tr Q8GNX9 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX9_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 11 EDDGFYMSAGYQIGEEAQM 30

tr Q8GNX7 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX7_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 11 EDDGFYMSAGYQIGEEAQM 30

tr Q8GNX5 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX5_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQMV 30

tr Q8GNX4 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX4_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQMV 30

tr Q8GNX3 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX3_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQMV 30

tr Q8GNX2 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX2_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQMV 30

tr Q8GNX1 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX1_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q8GNW9 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNW9_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q8GNW8 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNW8_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q8GNW7 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNW7_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q8GNW6 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNW6_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q8GNW5 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNW5_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q8GNW4 BabB (Fragment) [babB] [Helicobacter pylori] 137
Q8GNW4_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 13 EDDGFYMSAGYQIGEEAAQMV 32

tr Q8GNW3 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNW3_HELPY (Campylobacter
pylori)] AA
align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q7WVA5 Adhesin-binding fucosylated histo-blood group antigen 694
Q7WVA5_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q7WVA0 Adhesin-binding fucosylated histo-blood group antigen 696
Q7WVA0_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 13 EDDGFYMSAGYQIGEEAQM 32

tr Q7WV97 Adhesin-binding fucosylated histo-blood group antigen 694
Q7WV97_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 11 EDDGFYMSAGYQIGEEAQM 30

tr Q7WV96 Adhesin-binding fucosylated histo-blood group antigen 694
Q7WV96_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 11 EDDGFYMSAGYQIGEEAQM 30

tr Q7WV95 Adhesin-binding fucosylated histo-blood group antigen 695
Q7WV95_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 12 EDDGFYMSAGYQIGEEAQM 31

tr Q7WV94 Adhesin-binding fucosylated histo-blood group antigen 695
Q7WV94_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 12 EDDGFYMSAGYQIGEEAAQMV 31

tr Q7WV93 Adhesin-binding fucosylated histo-blood group antigen 694
Q7WV93_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q7WV92 Adhesin-binding fucosylated histo-blood group antigen 694
Q7WV92_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAAQMV 30

tr Q7WV90 Adhesin-binding fucosylated histo-blood group antigen 697
Q7WV90_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 13 EDDGFYMSAGYQIGEEAAQMV 32

tr Q7WV89 Adhesin-binding fucosylated histo-blood group antigen 697
Q7WV89_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 13 EDDGFYMSAGYQIGEEAQMV 32

tr [Q7WV88](#) Adhesin-binding fucosylated histo-blood group antigen 696
Q7WV88_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 13 EDDGFYMSAGYQIGEEAQMV 32

tr [Q7WV87](#) Adhesin-binding fucosylated histo-blood group antigen 694
Q7WV87_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQMV 30

tr [Q7WV86](#) Adhesin-binding fucosylated histo-blood group antigen 704
Q7WV86_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAQMV 40

tr [Q7WV85](#) Adhesin-binding fucosylated histo-blood group antigen 732
Q7WV85_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAAQMV 40

tr Q7WV83 Adhesin-binding fucosylated histo-blood group antigen 737
Q7WV83_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAAQMV 40

tr Q7WV82 Adhesin-binding fucosylated histo-blood group antigen 732
Q7WV82_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAAQMV 40

tr Q7WV80 Adhesin-binding fucosylated histo-blood group antigen 736
Q7WV80_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAAQMV 40

tr Q7WV79 Adhesin-binding fucosylated histo-blood group antigen 739
Q7WV79_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAAQMV 40

tr Q7WV75 Adhesin-binding fucosylated histo-blood group antigen 738
Q7WV75_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAQMV 40

tr Q7WV70 Adhesin-binding fucosylated histo-blood group antigen 733
Q7WV70_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAQMV 40

tr Q7WV68 Adhesin-binding fucosylated histo-blood group antigen 733
Q7WV68_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAQMV 40

tr Q7WV67 Adhesin-binding fucosylated histo-blood group antigen 734
Q7WV67_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFYMSAGYQIGEEAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAQMV 40

tr Q7WV66 Adhesin-binding fucosylated histo-blood group antigen 739
Q7WV66_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 21 EDDGFYMSAGYQIGEEAQM 40

tr Q6JAA1 Adhesin-binding fucosylated histo-blood group antigen 742
Q6JAA1_HELPY [babA] AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 21 EDDGFYMSAGYQIGEEAQM 40

tr Q6JAA0 Adhesin-binding fucosylated histo-blood group antigen 737
Q6JAA0_HELPY [babA] AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 21 EDDGFYMSAGYQIGEEAQM 40

tr Q6JA99 Adhesin-binding fucosylated histo-blood group antigen 741
Q6JA99_HELPY [babA] AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEAQM
Sbjct: 21 EDDGFYMSAGYQIGEEAQM 40

tr Q6JA98 Adhesin-binding fucosylated histo-blood group antigen 740
Q6JA98_HELPY [babA] AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEEAAQMV 40

tr [Q6JA97](#) Adhesin-binding fucosylated histo-blood group antigen 742
Q6JA97_HELPY [babA] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 69.4 bits (156), Expect = 7e-12
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMSAGYQIGEEAAQMV
Sbjct: 19 EDDGFYMSAGYQIGEEAAQMV 38

tr [Q6U2D5](#) Adhesin-binding fucosylated histo-blood group (Fragment) 137
Q6U2D5_HELPY [babB] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 66.8 bits (150), Expect = 4e-11
Identities = 19/20 (95%), Positives = 20/20 (100%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
ED+GFYMSAGYQIGEEAAQMV
Sbjct: 9 EDEGFYMSAGYQIGEEAAQMV 28

tr [Q8GNX6](#) BabB (Fragment) [babB] [Helicobacter pylori 135
Q8GNX6_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 66.4 bits (149), Expect = 5e-11
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMS GYQIGEEAAQMV
Sbjct: 11 EDDGFYMSTGYQIGEEAAQMV 30

tr [Q7WV98](#) Adhesin-binding fucosylated histo-blood group antigen 694
Q7WV98_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 66.4 bits (149), Expect = 5e-11
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMS GYQIGEEAQM
Sbjct: 11 EDDGFYMSTGYQIGEEAQM 30

tr Q8GNX8 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNX8_HELPY (Campylobacter pylori)] AA
[align](#)

Score = 66.0 bits (148), Expect = 7e-11
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGE AQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQM 30

tr Q7WVA3 Adhesin-binding fucosylated histo-blood group antigen 694
Q7WVA3_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 66.0 bits (148), Expect = 7e-11
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGE AQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQM 30

tr Q6U2D3 Adhesin-binding fucosylated histo-blood group (Fragment) 143
Q6U2D3_HELPY [babB] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 66.0 bits (148), Expect = 7e-11
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGE AQMV
Sbjct: 11 EDDGFYMSAGYQIGEEAQM 30

tr Q7WV78 Adhesin-binding fucosylated histo-blood group antigen 734
Q7WV78_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 64.3 bits (144), Expect = 2e-10
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFYMSAGYQIGEEA Q V
Sbjct: 21 EDDGFYMSAGYQIGEEA QVV 40

tr Q7WV76 Adhesin-binding fucosylated histo-blood group antigen 737
Q7WV76_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 64.3 bits (144), Expect = 2e-10
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEAQM V
Sbjct: 21 EDDGFYMSAGYQIGEEAQM V 40

tr Q7WV71 Adhesin-binding fucosylated histo-blood group antigen 734
Q7WV71_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 64.3 bits (144), Expect = 2e-10
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEAQM V
Sbjct: 21 EDDGFYMSAGYQIGEEAQM V 40

tr Q6U2C8 Adhesin-binding fucosylated histo-blood group (Fragment) 143
Q6U2C8_HELPY [babB] AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 63.0 bits (141), Expect = 6e-10
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEAQM V
Sbjct: 11 EDDGFYMSAGYQIGEEAQM V 30

tr Q8GNX0 BabB (Fragment) [babB] [Helicobacter pylori 135
Q8GNX0_HELPY (Campylobacter
pylori)] AA
align

Score = 61.7 bits (138), Expect = 1e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEAQM V
Sbjct: 11 EDDGFYMSAGYQIGEEAQM V 30

tr Q7WV91 Adhesin-binding fucosylated histo-blood group antigen 696
Q7WV91_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 61.7 bits (138), Expect = 1e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEA Q V
Sbjct: 13 EDDGFYMSAGYQIGEEASQV V 32

tr Q7WV77 Adhesin-binding fucosylated histo-blood group antigen 734
Q7WV77_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 61.7 bits (138), Expect = 1e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEA Q V
Sbjct: 21 EDDGFYMSAGYQIGEEASQV V 40

tr Q7WV73 Adhesin-binding fucosylated histo-blood group antigen 736
Q7WV73_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 61.7 bits (138), Expect = 1e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEA Q V
Sbjct: 21 EDDGFYMSAGYQIGEEASQV V 40

tr Q7WV72 Adhesin-binding fucosylated histo-blood group antigen 734
Q7WV72_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 61.7 bits (138), Expect = 1e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM V 20
EDDGFYMSAGYQIGEEA Q V
Sbjct: 21 EDDGFYMSAGYQIGEEASQV V 40

tr Q9ZKV2 Outer membrane protein-adhesin [babA] [Helicobacter 744
Q9ZKV2_HELPY pylori J99 AA
(Campylobacter pylori J99)] align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEEAAQMV 40

tr O25840 Outer membrane protein (Omp28) [HP1243] [Helicobacter 733
O25840_HELPY pylori AA
(Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEEAAQMV 40

tr O25556 Outer membrane protein (Omp19) [HP0896] [Helicobacter 708
O25556_HELPY pylori AA
(Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 20 EDDGFYTSVGYQIGEEAAQMV 39

tr O25086 Outer membrane protein (Omp9) [HP0317] [Helicobacter 745
O25086_HELPY pylori AA
(Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEEAAQMV 40

tr Q8GNW2 BabB (Fragment) [babB] [Helicobacter pylori 137
Q8GNW2_HELPY (Campylobacter AA
pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 13 EDDGFYTSVG YQIGEEAAQMV 32

tr Q8GNW1 BabB (Fragment) [babB] [Helicobacter pylori] 145
Q8GNW1_HELPY (Campylobacter
pylori)] AA
align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 20 EDDGFYTSVG YQIGEEAAQMV 39

tr Q8GNW0 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNW0_HELPY (Campylobacter
pylori)] AA
align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 11 EDDGFYTSVG YQIGEEAAQMV 30

tr Q8GNV8 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNV8_HELPY (Campylobacter
pylori)] AA
align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 11 EDDGFYTSVG YQIGEEAAQMV 30

tr Q8GNV7 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNV7_HELPY (Campylobacter
pylori)] AA
align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 11 EDDGFYTSVG YQIGEEAAQMV 30

tr Q8GNV6 BabB (Fragment) [babB] [Helicobacter pylori] 135
Q8GNV6_HELPY (Campylobacter
pylori)] AA
[align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFY S GYQIGEEAQM
Sbjct: 11 EDDGFYTSVG YQIGEEAQM 30

tr Q7WVA4 Adhesin-binding fucosylated histo-blood group antigen 704
Q7WVA4_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFY S GYQIGEEAQM
Sbjct: 21 EDDGFYTSVG YQIGEEAQM 40

tr Q7WVA2 Adhesin-binding fucosylated histo-blood group antigen 695
Q7WVA2_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFY S GYQIGEEAQM
Sbjct: 12 EDDGFYTSVG YQIGEEAQM 31

tr Q7WVA1 Adhesin-binding fucosylated histo-blood group antigen 695
Q7WVA1_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQM 20
EDDGFY S GYQIGEEAQM
Sbjct: 12 EDDGFYTSVG YQIGEEAQM 31

tr Q7WV99 Adhesin-binding fucosylated histo-blood group antigen 694
Q7WV99_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 11 EDDGFYTSVGYQIGEEAAQMV 30

tr Q7WV84 Adhesin-binding fucosylated histo-blood group antigen 739
Q7WV84_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEEAAQMV 40

tr Q7WV81 Adhesin-binding fucosylated histo-blood group antigen 737
Q7WV81_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEEAAQMV 40

tr Q7WV74 Adhesin-binding fucosylated histo-blood group antigen 736
Q7WV74_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFY S GYQIGEEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEEAAQMV 40

tr Q7WV69 Adhesin-binding fucosylated histo-blood group antigen 736
Q7WV69_HELPY (Fragment) AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFY S GYQIGEEAQMV
Sbjct: 21 EDDGFYTSVGYQIGEEAQMV 40

tr Q6T8D5 BabB (BabB2) [Helicobacter pylori (Campylobacter 706
Q6T8D5_HELPY pylori)] AA
[align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFY S GYQIGEEAQMV
Sbjct: 18 EDDGFYTSVGYQIGEEAQMV 37

tr Q6T8D3 BabA [Helicobacter pylori (Campylobacter pylori)] 742 AA
Q6T8D3_HELPY
[align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFY S GYQIGEEAQMV
Sbjct: 18 EDDGFYTSVGYQIGEEAQMV 37

tr Q5Q1P2 BabB/BabA1 fusion protein 1 (Fragment) [babB/babA1 731
Q5Q1P2_HELPY fusion] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFY S GYQIGEEAQMV
Sbjct: 18 EDDGFYTSVGYQIGEEAQMV 37

tr Q5Q1P1 BabB/BabA1 fusion protein 2 (Fragment) [babB/babA1 732
Q5Q1P1_HELPY fusion] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFY S GYQIGEEAQMV
Sbjct: 18 EDDGFYTSVG YQIGEEAQMV 37

tr Q52269 Adhesin binding fucosylated histo-blood group antigen 741
Q52269_HELPY [babA2] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFY S GYQIGEEAQMV
Sbjct: 21 EDDGFYTSVG YQIGEEAQMV 40

tr Q51811 Adhesin-binding fucosylated histo-blood group antigen 706
Q51811_HELPY [babB] AA
[Helicobacter pylori (Campylobacter pylori)] [align](#)

Score = 59.6 bits (133), Expect = 6e-09
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
EDDGFY S GYQIGEEAQMV
Sbjct: 18 EDDGFYTSVG YQIGEEAQMV 37

tr Q9ZN51 Putative Outer membrane protein [JHP0007] [Helicobacter 668
Q9ZN51_HELPJ pylori AA
J99 (Campylobacter pylori J99)] [align](#)

Score = 58.3 bits (130), Expect = 1e-08
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEEAQMV
Sbjct: 18 EDNGFFISAGYQIGEEAQMV 37

tr Q9X748 HopZ protein precursor [hopZ] [Helicobacter pylori 667
Q9X748_HELPY (Campylobacter AA
pylori)] [align](#)

Score = 58.3 bits (130), Expect = 1e-08
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEEAQMV
Sbjct: 19 EDNGFFISAGYQIGEEAQMV 38

tr [Q9X747](#) HopZ protein precursor [hopZ] [Helicobacter pylori] 669
Q9X747_HELPY (Campylobacter AA
pylori)] [align](#)

Score = 58.3 bits (130), Expect = 1e-08
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEEAQMV
Sbjct: 19 EDNGFFISAGYQIGEEAQMV 38

tr [Q9X746](#) HopZ protein precursor [hopZ] [Helicobacter pylori] 699
Q9X746_HELPY (Campylobacter AA
pylori)] [align](#)

Score = 58.3 bits (130), Expect = 1e-08
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEEAQMV
Sbjct: 19 EDNGFFISAGYQIGEEAQMV 38

tr [Q9X745](#) HopZ protein precursor [hopZ] [Helicobacter pylori] 668
Q9X745_HELPY (Campylobacter AA
pylori)] [align](#)

Score = 58.3 bits (130), Expect = 1e-08
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEEAQMV
Sbjct: 19 EDNGFFISAGYQIGEEAQMV 38

tr [Q9S3I7](#) HopZ protein precursor [hopZ] [Helicobacter pylori] 666
Q9S3I7_HELPY (Campylobacter AA
pylori)] [align](#)

Score = 58.3 bits (130), Expect = 1e-08
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEEAQMV
Sbjct: 19 EDNGFFISAGYQIGEEAQMV 38

tr Q7X2J7 HopZ (Fragment) [hopZ] [Helicobacter pylori] 73 AA
Q7X2J7_HELPY (Campylobacter
pylori)] align

Score = 58.3 bits (130), Expect = 1e-08
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
ED+GF+ SAGYQIGEEAAQMV
Sbjct: 17 EDNGFFISAGYQIGEEAAQMV 36

tr Q9Z390 Putative Outer membrane protein [JHP0212] [Helicobacter] 696
Q9Z390_HELPJ pylori AA
J99 (Campylobacter pylori J99)] align

Score = 57.1 bits (127), Expect = 4e-08
Identities = 17/20 (85%), Positives = 17/20 (85%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
EDDGFYMS GYQIGEA Q V
Sbjct: 22 EDDGFYMSVGYQIGEEAVQKV 41

tr Q5G5J5 Adhesin-binding fucosylated histo-blood group (Fragment) 138
Q5G5J5_HELPY [babB] AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 57.1 bits (127), Expect = 4e-08
Identities = 17/20 (85%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
E+DGFY S GYQIGEEAAQMV
Sbjct: 9 ENDGFYTSVGYQIGEEAAQMV 28

tr Q6U2C5 Adhesin-binding fucosylated histo-blood group (Fragment) 134
Q6U2C5_HELPY [babB] AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 57.1 bits (127), Expect = 4e-08
Identities = 17/20 (85%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
E+DGFY S GYQIGEEAAQMV
Sbjct: 11 ENDGFYTSVGYQIGEEAAQMV 30

tr Q9ZMK5 Outer membrane protein/porin [hopA] [Helicobacter pylori] 483
Q9ZMK5_HELPJ J99 AA
(Campylobacter pylori J99)] align

Score = 56.2 bits (125), Expect = 6e-08
Identities = 17/20 (85%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
E+DG YMS GYQIGEEAAQMV
Sbjct: 17 ENDGVYMSVGYQIGEEAAQMV 36

tr Q9ZN38 Putative Outer membrane protein [JHP0021] [Helicobacter 690
Q9ZN38_HELPJ pylori AA
J99 (Campylobacter pylori J99)] [align](#)

Score = 55.8 bits (124), Expect = 8e-08
Identities = 16/20 (80%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
ED+GF+ SAGYQIGE AQMV
Sbjct: 21 EDNGFFVSAGYQIGESAQMV 40

tr O24870 Outer membrane protein (Omp2) [HP0025] [Helicobacter 711
O24870_HELPJ pylori AA
(Campylobacter pylori)] [align](#)

Score = 55.8 bits (124), Expect = 8e-08
Identities = 16/20 (80%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
ED+GF+ SAGYQIGE AQMV
Sbjct: 21 EDNGFFVSAGYQIGESAQMV 40

tr Q9ZLC1 Putative Outer membrane protein [JHP0659] [Helicobacter 638
Q9ZLC1_HELPJ pylori AA
J99 (Campylobacter pylori J99)] [align](#)

Score = 54.9 bits (122), Expect = 2e-07
Identities = 16/20 (80%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAAQMV 20
ED+GF+ SAGYQIGEA QMV
Sbjct: 21 EDNGFFVSAGYQIGEAQMV 40

tr Q9ZLB8 Putative Outer membrane protein [JHP0662] [Helicobacter 651
Q9ZLB8_HELPJ pylori AA
J99 (Campylobacter pylori J99)] [align](#)

Score = 54.9 bits (122), Expect = 2e-07
Identities = 16/20 (80%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEA QMV
Sbjct: 21 EDNGFFVSAGYQIGEAVQMV 40

tr Q7X2K7 SabA (Fragment) [sabA] [Helicobacter pylori] 99 AA
Q7X2K7_HELPY (Campylobacter
pylori)] align

Score = 54.9 bits (122), Expect = 2e-07
Identities = 16/20 (80%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEA QMV
Sbjct: 19 EDNGFFVSAGYQIGEAVQMV 38

tr Q7X2K6 SabA (Fragment) [sabA] [Helicobacter pylori] 99 AA
Q7X2K6_HELPY (Campylobacter
pylori)] align

Score = 54.9 bits (122), Expect = 2e-07
Identities = 16/20 (80%), Positives = 18/20 (90%)

Query: 1 EDDGFYMSAGYQIGEEAQMV 20
ED+GF+ SAGYQIGEA QMV
Sbjct: 19 EDNGFFVSAGYQIGEAVQMV 38

Database: EXPASY/UniProtKB

Posted date: Apr 28, 2005 3:30 PM

Number of letters in database: 604,459,357

Number of sequences in database: 1,880,849

Lambda	K	H
0.334	0.275	1.76

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of HSP's successfully gapped in prelim test: 0

length of query: 20

length of database: 604,459,357

effective HSP length: 11

effective length of query: 9

effective length of database: 583,770,018

effective search space: 5253930162

effective search space used: 5253930162

T: 16

A: 40

X1: 15 (7.2 bits)

X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 41 (21.6 bits)
S2: 61 (29.1 bits)

Wallclock time: 7 seconds

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DOCUMENT-IDENTIFIER: US 6887663 B1

TITLE: Streptococcus pneumoniae SP036 polynucleotides

Detailed Description Paragraph Table (7):

ACGAGTAAAAAGCGAA SP075 amino acid (SEQ ID NO:126)

YYLSRES DLEVTVFDHEQGQATKAAAGIISPWF SKRRNKAWYKMARLGADFYVDLLADLEKSC
QRSGVFLKKDES NLEELYQLALQRREESPLIGQLAILNQASANELFPGLQGFDRLLYASGGARV
LVTRLLEVSHVKLVKEKVTLTPLASGYOIGEEFEQVILATGAWLGDMLEPLGYEVDVRPQRC
LAQDMEDYPVVMPEGEWDLIPFAGGKLSLGATHENDMGFDLTVDETLLQQMEEATLTHYLILA
ERVGIRAYTSDFS PFFGQVPDLTG VYAASGLGSSGLTTGP IIGYHLAQLIQDKELTLDPLNYPIN
RVKSE SP076 nucleotide (SEQ ID NO:127)

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DATE: Tuesday, May 03, 2005

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	<i>DB=USPT; PLUR=YES; OP=AND</i>		
<input type="checkbox"/>	L1	blood near2 group near2 binding near2 protein	4
<input type="checkbox"/>	L2	antiadhesion or anti-adhesion or anti-adhesin or antiadhesin or antibab or antibaba or anti-bab or anti-bab-a or antibab\$3	963
<input type="checkbox"/>	L3	L2 and helicobacter	12
<input type="checkbox"/>	L4	L3 not l1	12
<input type="checkbox"/>	L5	L3 not l1	12
<input type="checkbox"/>	L6	antibab or antibaba or anti-bab or anti-bab-a or antibab\$3	6
<input type="checkbox"/>	L7	helicobacter near10 (adhesin or adherence or attachment or receptor)	56
<input type="checkbox"/>	L8	L7 and (blood or lewis)	51
<input type="checkbox"/>	L9	L7 same (blood or lewis)	17
<input type="checkbox"/>	L10	antihelicobacter	1

END OF SEARCH HISTORY

6843993. 27 Jul 01; 18 Jan 05. Anti-microbial-adhesion fraction derived from vaccinium. Ofek; Itzhak, et al. 424/732; 424/405 424/408 424/410 424/417 424/440 424/777. A01N065/00 A61K035/78.

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Terms	Documents
L3 not L1	12

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File 155:MEDLINE(R) 1951-2005/May W1
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Set Items Description

Cost is in DialUnits
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Set	Items	Description
S1	413	'BABA PROTEIN, HELICOBACTER PYLORI' OR 'BAB' OR 'BABA'
S2	52	S1 AND HELICOBACT?
S3	52	S2/1997:2005
S4	0	S2 NOT S3
S5	10	E3-E4
S6	10	S5/1997:2005
S7	17	PORIN? AND HELICOBACTER?
S8	11	S7/1997:2005
S9	6	S7 NOT S8
S10	305	'HOPF'
S11	69	'HOPG'
S12	4	'HOPH'
S13	57	'HOPI'
S14	10	'HOPZ' OR 'HOPZ PROTEIN, HELICOBACTER PYLORI'
S15	3	'HOPQ'
S16	447	S10 OR S11 OR S12 OR S13 OR S14 OR S15
S17	1454	S16 OR HOP
S18	924	S17/1997:2005
S19	530	S17 NOT S18
S20	0	S19 AND (PYLORI OR PYLORIS OR PYLROI OR PYLORIDIS OR HELIC-OBAC?)
S21	4328	PORIN? OR HOP
S22	20	S21 AND (PYLORI OR PYLORIS OR PYLROI OR PYLORIDIS OR HELIC-OBAC?)
S23	14	S22/1997:2005
S24	6	S22 NOT S23

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24/9/1

DIALOG(R) File 155:MEDLINE(R)
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11140349 PMID: 7559328

Isolation and characterization of a conserved porin protein from Helicobacter pylori .

Doig P; Exner M M; Hancock R E; Trust T J

Canadian Bacterial Diseases Network, University of Victoria, British Columbia, Canada.

Journal of bacteriology (UNITED STATES) Oct 1995, 177 (19) p5447-52, ISSN 0021-9193 Journal Code: 2985120R

Contract/Grant No.: R01A129927-01A2; PHS

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Helicobacter pylori is a causative agent of gastritis in humans and

is correlated with gastric ulcer formation. Infections with this bacterium have proven difficult to treat with antimicrobial agents. To better understand how this bacterium transports compounds such as antimicrobial agents across its outer membrane, identification of **porin** proteins is important. We have recently identified a family of *H. pylori* **porins** (HopA to HopD) (M. M. Exner, P. Doig, T. J. Trust, and R. E. W. Hancock, Infect. Immun. 63:1567-1572, 1995). Here, we report on an unrelated **porin** species (HopE) from this bacterium. This protein had a apparent molecular mass of 31 kDa and was seen to form 50- and 90-kDa aggregates that were designated putative dimeric and trimeric forms, respectively. The protein was purified to homogeneity and, with a model planar lipid membrane system, was shown to act as a nonselective pore with a single channel conductance in 1.0 M KCl of 1.5 nS, similarly to other bacterial nonspecific **porins**. An internal peptide sequence of HopE shared homology with the P2 **porin** of *Haemophilus influenzae*. HopE was also shown to be antigenic in vivo as assessed by sera taken from *H. pylori* -infected individuals and was immunologically conserved with both patient sera and specific monoclonal antibodies. From these data, it appears that HopE is a major nonselective **porin** of *H. pylori*. The implications of these findings are discussed.

Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.

Descriptors: ***Helicobacter** r **pylori** --chemistry--CH; *** Porins** --chemistry--CH; Amino Acid Sequence; Antibodies, Bacterial; Antibodies, Monoclonal; Cross-Linking Reagents; Electric Conductivity; **Helicobacter pylori** --immunology--IM; Humans; Lipid Bilayers; Membrane Potentials; Molecular Sequence Data; Molecular Weight; Peptide Fragments--chemistry--CH; **Porins** --immunology--IM; **Porins** --isolation and purification--IP; Sequence Analysis; Sequence Homology, Amino Acid; Succinimides
CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antibodies, Monoclonal); 0 (Cross-Linking Reagents); 0 (Lipid Bilayers); 0 (Peptide Fragments); 0 (Porins); 0 (Succinimides); 57757-57-0 (dithiobis(succinimidylpropionate))
Record Date Created: 19951106
Record Date Completed: 19951106

24/9/2

DIALOG(R) File 155:MEDLINE(R)

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11024097 PMID: 7600133

Progress in defining the inflammatory cascade.

Figura N

School of Gastroenterology, University of Siena, Policlinico Le Scotte, Italy.

European journal of gastroenterology & hepatology (ENGLAND) Apr 1995,

7 (4) p296-302, ISSN 0954-691X Journal Code: 9000874

Publishing Model Print

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Helicobacter pylori infection is characterized by an inflammatory response in the gastric epithelium, the intensity of which appears to be type-strain specific. Infections caused by Type 1 *H. pylori* organisms, i.e., those expressing VacA (the cytotoxin) and CagA (the cytotoxin-associated protein), are associated with a strong polymorph

mucosal infiltration in vivo, and with increased secretion of interleukin-8 by epithelial cells. The inflammatory potential of Type II strains (non-cytotoxic, VacA- and CagA-negative) is probably less pronounced. The small urease subunit, porins, and other substances produced by H. pylori show neutrophil chemotactic activities in vitro. These bacterial components promote the adhesion of polymorphs to endothelial cells and stimulate polymorphs to generate oxygen reactive metabolites. This can severely damage the gastroduodenal mucosa. (38 Refs.)

Descriptors: *Helicobacter Infections--metabolism--ME; * Helicobacter pylori ; Helicobacter pylori --metabolism--ME; Humans; Inflammation --metabolism--ME; Interleukin-8--metabolism--ME

CAS Registry No.: 0 (Interleukin-8)

Record Date Created: 19950807

Record Date Completed: 19950807

24/9/3

DIALOG(R) File 155:MEDLINE(R)

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10992393 PMID: 7773243

Cell surface characteristics of Helicobacter pylori .

Moran A P

Department of Microbiology, University College, Galway, Ireland.

FEMS immunology and medical microbiology (NETHERLANDS) Feb 1995, 10 (3-4) p271-80, ISSN 0928-8244 Journal Code: 9315554

Publishing Model Print

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Helicobacter pylori is an important gastroduodenal pathogen of humans. Immunological and structural studies have been performed on the phospholipids, lipopolysaccharides (LPS) and some surface proteins of H. pylori strains. H. pylori LPS has, in general, low immunological activity and this property may aid the survival of this chronic infection. Nevertheless, H. pylori LPS has been found to influence the quality of gastric mucin and to stimulate pepsinogen secretion, thereby contributing to gastric disease. A number of putative adhesins of the bacterium have been described. This multiplicity of adhesins may reflect that H. pylori adherence is a multi-step process involving different interactions, and that different adhesins may mediate adherence to various sites in gastric tissue. (54 Refs.)

Tags: Research Support, Non-U.S. Gov't

Descriptors: *Bacterial Outer Membrane Proteins--chemistry--CH; * Helicobacter pylori --physiology--PH; *Lipopolysaccharides--chemistry --CH; *Lipopolysaccharides--immunology--IM; Adhesins, Bacterial--chemistry --CH; Adhesins, Bacterial--physiology--PH; Animals; Bacterial Capsules --physiology--PH; Bacterial Outer Membrane Proteins--physiology--PH; Carbohydrate Sequence; Cell Wall--chemistry--CH; Cell Wall--physiology--PH ; Heat-Shock Proteins--chemistry--CH; Helicobacter pylori --pathogenicity--PY; Humans; Molecular Sequence Data; Porins --chemistry --CH; Porins --immunology--IM; Rats

CAS Registry No.: 0 (Adhesins, Bacterial); 0 (Bacterial Capsules); 0 (Bacterial Outer Membrane Proteins); 0 (Heat-Shock Proteins); 0 (Lipopolysaccharides); 0 (Porins)

Record Date Created: 19950713

Record Date Completed: 19950713

24/9/4

DIALOG(R) File 155:MEDLINE(R)

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10899919 PMID: 7534278

Isolation and characterization of a family of porin proteins from *Helicobacter pylori*.

Exner M M; Doig P; Trust T J; Hancock R E

Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.

Infection and immunity (UNITED STATES) Apr 1995, 63 (4) p1567-72,
ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: R01AI29927-01A2; AI; NIAID

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Two-dimensional gel electrophoresis was used to identify heat-modifiable outer membrane proteins, which were candidates for **porins**, from *Helicobacter pylori* membrane preparations. Four such proteins with apparent molecular masses of 48, 49, 50, and 67 kDa were isolated. The four proteins copurified together after selective detergent solubilizations followed by anion-exchange chromatography, and each protein was ultimately purified to homogeneity by gel purification. These proteins were then tested for pore-forming ability with a planar lipid bilayer model membrane system. All four proteins appeared to be present as monomers, and they formed pores with low single-channel conductances in 1.0 M KCl of 0.36, 0.36, 0.30, and 0.25 nS, respectively, for the 48-, 49-, 50-, and 67-kDa proteins which we propose to designate HopA, HopB, HopC, and HopD. N-terminal amino acid sequence analyses showed a high degree of homology among all four proteins, and it appears that these proteins constitute a family of related **porins** in *H. pylori*.

Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.

Descriptors: ***Helicobacter pylori** --chemistry--CH; *** Porins** --isolation and purification--IP; Amino Acid Sequence; Electric Conductivity; Electrophoresis, Gel, Two-Dimensional; Heat; **Helicobacter pylori** --physiology--PH; Ion Channels--chemistry--CH; Ion Channels --isolation and purification--IP; Molecular Sequence Data; Molecular Weight ; Multigene Family; **Porins** --chemistry--CH; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 0 (Ion Channels); 0 (Porins)

Gene Symbol: hopA; hopB; hopC; hopD

Record Date Created: 19950420

Record Date Completed: 19950420

24/9/5

DIALOG(R) File 155:MEDLINE(R)

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10721188 PMID: 7927718

Identification of surface-exposed outer membrane antigens of

Helicobacter pylori .

Doig P; Trust T J

Department of Biochemistry and Microbiology, University of Victoria,
British Columbia, Canada.

Infection and immunity (UNITED STATES) Oct 1994, 62 (10) p4526-33,
ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: 1R01AI29927-01A2; AI; NIAID

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Despite the potential significance of surface-localized antigens in the colonization by and disease processes of *Helicobacter pylori* , few such components have been unequivocally identified and/or characterized. To further investigate the surface of this bacterium, monoclonal antibodies (MAbs) to a sarcosine-insoluble outer membrane fraction prepared from *H. pylori* NCTC 11637 were raised. MAbs were selected on the basis of their surface reactivity to whole cells by enzyme-linked immunosorbent assay, immunofluorescence, and immunoelectron microscopy. By use of this selection protocol, 14 surface-reactive MAbs were chosen. These MAbs were used to identify six protein antigens (molecular masses, 80, 60, 51, 50, 48, and 31 kDa), all of which were localized within or associated with the outer membrane. Two of the MAbs recognized the core region of lipopolysaccharide (LPS). Only these two anti-LPS MAbs also recognized the flagellar sheath, indicating a structural difference between the sheath and outer membrane. Three of the protein antigens (80, 60, and 51 kDa) were strain specific, while the other three antigens were present in other strains of *H. pylori* . Both the 51- and 48-kDa antigens were heat modifiable and likely are porins . A conserved 31-kDa protein may represent another species of porin . A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of *H. pylori* outer membranes with minimal inner membrane contamination is described. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis showed that the protein content of the *H. pylori* outer membrane is similar structurally to those of other species of *Helicobacter* but markedly different from those of taxonomically related *Campylobacter* spp. and *Escherichia coli* . *H. pylori* also appeared to lack peptidoglycan-associated proteins.

Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.

Descriptors: *Antigens, Bacterial--analysis--AN; *Bacterial Outer Membrane Proteins--analysis--AN; **Helicobacter pylori* --immunology--IM; Animals; Antibodies, Monoclonal--immunology--IM; Antigens, Surface--analysis--AN; Mice; Mice, Inbred BALB C; Molecular Weight

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial); 0 (Antigens, Surface); 0 (Bacterial Outer Membrane Proteins)

Record Date Created: 19941104

Record Date Completed: 19941104

24/9/6

DIALOG(R) File 155:MEDLINE(R)

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10540278 PMID: 8132346

Immunobiological activities of *Helicobacter pylori* porins .

Tufano M A; Rossano F; Catalanotti P; Liguori G; Capasso C; Ceccarelli M

T; Marinelli P

Istituto di Microbiologia, Seconda Universita di Napoli, Italy.

Infection and immunity (UNITED STATES) Apr 1994, 62 (4) p1392-9,
ISSN 0019-9567 Journal Code: 0246127

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with H. **pylori porins** showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of H. **pylori porins** released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 microgram/ml/10(6) cells. Interleukin-6 (IL-6) appears later, with a peak at 10 micrograms/ml/10(6) cells, while IL-8 is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells, while IL-8 is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells. Lymphocytes stimulated by H. **pylori porins** release gamma interferon after 18 h of culture at higher concentrations of **porins** (20 micrograms/ml/10(6) cells). Granulocyte macrophage colony-stimulating factor is released from 6 to 48 h at a concentration of 1 microgram/ml/10(6) cells, while both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 microgram/ml/10(6) cells, respectively). Our results lead us to think that during H. **pylori** infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory to the immunological responses.

Tags: Research Support, Non-U.S. Gov't

Descriptors: ***Helicobacter pylori** --pathogenicity--PY; * **Porins** --pharmacology--PD; Chemotaxis, Leukocyte--drug effects--DE; Granulocyte-Macrophage Colony-Stimulating Factor--secretion--SE; Humans; Interleukins --secretion--SE; Lymphocytes--drug effects--DE; Lymphocytes--secretion--SE; Monocytes--drug effects--DE; Monocytes--secretion--SE; Neutrophils--drug effects--DE; Neutrophils--immunology--IM; Tumor Necrosis Factor-alpha --secretion--SE

CAS Registry No.: 0 (Interleukins); 0 (Porins); 0 (Tumor Necrosis Factor-alpha); 83869-56-1 (Granulocyte-Macrophage Colony-Stimulating Factor)

Record Date Created: 19940421

Record Date Completed: 19940421

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\$2.28 Estimated total session cost 0.239 DialUnits

11140349 PMID: 7559328

Isolation and characterization of a conserved porin protein from Helicobacter pylori.

Doig P; Exner M M; Hancock R E; Trust T J

Canadian Bacterial Diseases Network, University of Victoria, British Columbia, Canada.

Journal of bacteriology (UNITED STATES) Oct 1995, 177 (19) p5447-52, ISSN 0021-9193 Journal Code: 2985120R

Contract/Grant No.: R01A129927-01A2; PHS

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Helicobacter pylori is a causative agent of gastritis in humans and is correlated with gastric ulcer formation. Infections with this bacterium have proven difficult to treat with antimicrobial agents. To better understand how this bacterium transports compounds such as antimicrobial agents across its outer membrane, identification of **porin** proteins is important. We have recently identified a family of *H. pylori* **porins** (HopA to HopD) (M. M. Exner, P. Doig, T. J. Trust, and R. E. W. Hancock, Infect. Immun. 63:1567-1572, 1995). Here, we report on an unrelated **porin** species (HopE) from this bacterium. This protein had a apparent molecular mass of 31 kDa and was seen to form 50- and 90-kDa aggregates that were designated putative dimeric and trimeric forms, respectively. The protein was purified to homogeneity and, with a model planar lipid membrane system, was shown to act as a nonselective pore with a single channel conductance in 1.0 M KCl of 1.5 nS, similarly to other bacterial nonspecific **porins**. An internal peptide sequence of HopE shared homology with the P2 **porin** of Haemophilus influenzae. HopE was also shown to be antigenic in vivo as assessed by sera taken from *H. pylori*-infected individuals and was immunologically conserved with both patient sera and specific monoclonal antibodies. From these data, it appears that HopE is a major nonselective **porin** of *H. pylori*. The implications of these findings are discussed.

Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.

Descriptors: ***Helicobacter pylori**--chemistry--CH; * **Porins** --chemistry--CH; Amino Acid Sequence; Antibodies, Bacterial; Antibodies, Monoclonal; Cross-Linking Reagents; Electric Conductivity; **Helicobacter pylori** --immunology--IM; Humans; Lipid Bilayers; Membrane Potentials; Molecular Sequence Data; Molecular Weight; Peptide Fragments--chemistry--CH; **Porins** --immunology--IM; **Porins** --isolation and purification--IP; Sequence Analysis; Sequence Homology, Amino Acid; Succinimides

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antibodies, Monoclonal); 0 (Cross-Linking Reagents); 0 (Lipid Bilayers); 0 (Peptide Fragments); 0 (Porins); 0 (Succinimides); 57757-57-0 (dithiobis(succinimidylpropionate))

Record Date Created: 19951106

Record Date Completed: 19951106

9/9/2

DIALOG(R) File 155:MEDLINE(R)

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11024097 PMID: 7600133

Progress in defining the inflammatory cascade.

Figura N

School of Gastroenterology, University of Siena, Policlinico Le Scotte, Italy.

European journal of gastroenterology & hepatology (ENGLAND) Apr 1995,
7 (4) p296-302, ISSN 0954-691X Journal Code: 9000874

Publishing Model Print

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Helicobacter pylori infection is characterized by an inflammatory response in the gastric epithelium, the intensity of which appears to be type-strain specific. Infections caused by Type I *H. pylori* organisms, i.e., those expressing VacA (the cytotoxin) and CagA (the cytotoxin-associated protein), are associated with a strong polymorph mucosal infiltration in vivo, and with increased secretion of interleukin-8 by epithelial cells. The inflammatory potential of Type II strains (non-cytotoxic, VacA- and CagA-negative) is probably less pronounced. The small urease subunit, **porins**, and other substances produced by *H. pylori* show neutrophil chemotactic activities in vitro. These bacterial components promote the adhesion of polymorphs to endothelial cells and stimulate polymorphs to generate oxygen reactive metabolites. This can severely damage the gastroduodenal mucosa. (38 Refs.)

Descriptors: ***Helicobacter** r Infections--metabolism--ME; * **Helicobacter pylori**; **Helicobacter pylori**--metabolism--ME; Humans; Inflammation --metabolism--ME; Interleukin-8--metabolism--ME

CAS Registry No.: 0 (Interleukin-8)

Record Date Created: 19950807

Record Date Completed: 19950807

9/9/3

DIALOG(R) File 155:MEDLINE(R)

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10992393 PMID: 7773243

Cell surface characteristics of Helicobacter pylori.

Moran A P

Department of Microbiology, University College, Galway, Ireland.

FEMS immunology and medical microbiology (NETHERLANDS) Feb 1995, 10
(3-4) p271-80, ISSN 0928-8244 Journal Code: 9315554

Publishing Model Print

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Helicobacter pylori is an important gastroduodenal pathogen of humans. Immunological and structural studies have been performed on the phospholipids, lipopolysaccharides (LPS) and some surface proteins of *H. pylori* strains. *H. pylori* LPS has, in general, low immunological activity and this property may aid the survival of this chronic infection. Nevertheless, *H. pylori* LPS has been found to influence the quality of gastric mucin and to stimulate pepsinogen secretion, thereby contributing to gastric disease. A number of putative adhesins of the bacterium have been described. This multiplicity of adhesins may reflect that *H. pylori* adherence is a multi-step process involving different interactions, and that different adhesins may mediate adherence to various sites in gastric

tissue. (54 Refs.)

Tags: Research Support, Non-U.S. Gov't

Descriptors: *Bacterial Outer Membrane Proteins--chemistry--CH; ***Helicobacter pylori**--physiology--PH; *Lipopolysaccharides--chemistry--CH; *Lipopolysaccharides--immunology--IM; Adhesins, Bacterial--chemistry--CH; Adhesins, Bacterial--physiology--PH; Animals; Bacterial Capsules--physiology--PH; Bacterial Outer Membrane Proteins--physiology--PH; Carbohydrate Sequence; Cell Wall--chemistry--CH; Cell Wall--physiology--PH; Heat-Shock Proteins--chemistry--CH; **Helicobacter pylori**--pathogenicity--PY; Humans; Molecular Sequence Data; **Porins**--chemistry--CH; **Porins**--immunology--IM; Rats

CAS Registry No.: 0 (Adhesins, Bacterial); 0 (Bacterial Capsules); 0 (Bacterial Outer Membrane Proteins); 0 (Heat-Shock Proteins); 0 (Lipopolysaccharides); 0 (Porins)

Record Date Created: 19950713

Record Date Completed: 19950713

9/9/4

DIALOG(R) File 155:MEDLINE(R)

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10899919 PMID: 7534278

Isolation and characterization of a family of porin proteins from Helicobacter pylori.

Exner M M; Doig P; Trust T J; Hancock R E

Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.

Infection and immunity (UNITED STATES) Apr 1995, 63 (4) p1567-72, ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: R01AI29927-01A2; AI; NIAID

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Two-dimensional gel electrophoresis was used to identify heat-modifiable outer membrane proteins, which were candidates for **porins**, from **Helicobacter pylori** membrane preparations. Four such proteins with apparent molecular masses of 48, 49, 50, and 67 kDa were isolated. The four proteins copurified together after selective detergent solubilizations followed by anion-exchange chromatography, and each protein was ultimately purified to homogeneity by gel purification. These proteins were then tested for pore-forming ability with a planar lipid bilayer model membrane system. All four proteins appeared to be present as monomers, and they formed pores with low single-channel conductances in 1.0 M KCl of 0.36, 0.36, 0.30, and 0.25 nS, respectively, for the 48-, 49-, 50-, and 67-kDa proteins which we propose to designate HopA, HopB, HopC, and HopD. N-terminal amino acid sequence analyses showed a high degree of homology among all four proteins, and it appears that these proteins constitute a family of related **porins** in *H. pylori*.

Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.

Descriptors: ***Helicobacter pylori**--chemistry--CH; * **Porins**--isolation and purification--IP; Amino Acid Sequence; Electric Conductivity; Electrophoresis, Gel, Two-Dimensional; Heat; **Helicobacter pylori**--physiology--PH; Ion Channels--chemistry--CH; Ion Channels--isolation and purification--IP; Molecular Sequence Data; Molecular Weight; Multigene

Family; **Porins** --chemistry--CH; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 0 (Ion Channels); 0 (Porins)

Gene Symbol: hopA; hopB; hopC; hopD

Record Date Created: 19950420

Record Date Completed: 19950420

9/9/5

DIALOG(R) File 155:MEDLINE(R)

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10721188 PMID: 7927718

Identification of surface-exposed outer membrane antigens of Helicobacter pylori.

Doig P; Trust T J

Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Infection and immunity (UNITED STATES) Oct 1994, 62 (10) p4526-33, ISSN 0019-9567 Journal Code: 0246127

Contract/Grant No.: 1R01AI29927-01A2; AI; NIAID

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Subfile: INDEX MEDICUS

Despite the potential significance of surface-localized antigens in the colonization by and disease processes of **Helicobacter pylori**, few such components have been unequivocally identified and/or characterized. To further investigate the surface of this bacterium, monoclonal antibodies (MAbs) to a sarcosine-insoluble outer membrane fraction prepared from *H. pylori* NCTC 11637 were raised. MAbs were selected on the basis of their surface reactivity to whole cells by enzyme-linked immunosorbent assay, immunofluorescence, and immunoelectron microscopy. By use of this selection protocol, 14 surface-reactive MAbs were chosen. These MAbs were used to identify six protein antigens (molecular masses, 80, 60, 51, 50, 48, and 31 kDa), all of which were localized within or associated with the outer membrane. Two of the MAbs recognized the core region of lipopolysaccharide (LPS). Only these two anti-LPS MAbs also recognized the flagellar sheath, indicating a structural difference between the sheath and outer membrane. Three of the protein antigens (80, 60, and 51 kDa) were strain specific, while the other three antigens were present in other strains of *H. pylori*. Both the 51- and 48-kDa antigens were heat modifiable and likely are **porins**. A conserved 31-kDa protein may represent another species of **porin**. A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of *H. pylori* outer membranes with minimal inner membrane contamination is described. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis showed that the protein content of the *H. pylori* outer membrane is similar structurally to those of other species of **Helicobacter** but markedly different from those of taxonomically related *Campylobacter* spp. and *Escherichia coli*. *H. pylori* also appeared to lack peptidoglycan-associated proteins.

Tags: Research Support, Non-U.S. Gov't; Research Support, U.S. Gov't, P.H.S.

Descriptors: *Antigens, Bacterial--analysis--AN; *Bacterial Outer Membrane Proteins--analysis--AN; * **Helicobacter pylori**--immunology--IM; Animals; Antibodies, Monoclonal--immunology--IM; Antigens, Surface--analysis--AN; Mice; Mice, Inbred BALB C; Molecular Weight

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial)
; 0 (Antigens, Surface); 0 (Bacterial Outer Membrane Proteins)
Record Date Created: 19941104
Record Date Completed: 19941104

9/9/6

DIALOG(R) File 155:MEDLINE(R)

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10540278 PMID: 8132346

Immunobiological activities of Helicobacter pylori porins .

Tufano M A; Rossano F; Catalanotti P; Liguori G; Capasso C; Ceccarelli M
T; Marinelli P

Istituto di Microbiologia, Seconda Universita di Napoli, Italy.

Infection and immunity (UNITED STATES) Apr 1994, 62 (4) p1392-9,

ISSN 0019-9567 Journal Code: 0246127

Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

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Studies were carried out on some biological activities of **Helicobacter pylori porins** in vitro. We extracted and purified a **porin** with an apparent molecular mass of 30 kDa. Human polymorphonuclear leukocytes preincubated with **H. pylori porins** showed a decrease of chemotaxis, of adherence to nylon wool, and of chemiluminescence. Used as chemotaxins in place of zymosan-activated serum or as chemotaxinogens in place of zymosan, the **porins** induced polymorphonuclear leukocyte migration. Human monocytes and lymphocytes cultivated in the presence of **H. pylori porins** released cytokines. Release of the various cytokines studied was obtained with differentiated kinetics and at various **porin** concentrations. Starting only 3 h after culture, tumor necrosis factor alpha is released quickly, reaching a peak at 18 h, at a **porin** concentration of 1 microgram/ml/10(6) cells. Interleukin-6 (IL-6) appears later, with a peak at 10 micrograms/ml/10(6) cells, while IL-8 is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells, while IL-8 is released after 6 h of culture, with a peak at 24 h, at a **porin** concentration of 10 micrograms/ml/10(6) cells. Lymphocytes stimulated by **H. pylori porins** release gamma interferon after 18 h of culture at higher concentrations of **porins** (20 micrograms/ml/10(6) cells). Granulocyte macrophage colony-stimulating factor is released from 6 to 48 h at a concentration of 1 microgram/ml/10(6) cells, while both IL-3 and IL-4 are released after 18 h of culture at different **porin** concentrations (0.1 and 1 microgram/ml/10(6) cells, respectively). Our results lead us to think that during **H. pylori** infection, surface components, **porins** in particular, are able to induce a series of chain reactions ranging from the inflammatory to the immunological responses.

Tags: Research Support, Non-U.S. Gov't

Descriptors: ***Helicobacte** r **pylori**--pathogenicity--PY; * **Porins**--pharmacology--PD; Chemotaxis, Leukocyte--drug effects--DE; Granulocyte-Macrophage Colony-Stimulating Factor--secretion--SE; Humans; Interleukins--secretion--SE; Lymphocytes--drug effects--DE; Lymphocytes--secretion--SE; Monocytes--drug effects--DE; Monocytes--secretion--SE; Neutrophils--drug effects--DE; Neutrophils--immunology--IM; Tumor Necrosis Factor-alpha--secretion--SE

CAS Registry No.: 0 (Interleukins); 0 (Porins); 0 (Tumor Necrosis

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- ☐ 1. [6828298](#). 13 Apr 01; 07 Dec 04. Glycoprotein having inhibitory activity against helicobacter pylori colonization. Kodama; Yoshikatsu, et al. 514/8; 424/9.1 435/252.1 530/395 530/413. A61K038/16 A61K049/00.
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- ☐ 5. [6576625](#). 16 Mar 01; 10 Jun 03. Targeted vesicular constructs for cytoprotection and treatment of H. pylori infections. Singh; Amarjit, et al. 514/78; 514/152 514/182 514/192. A61K031/685 A61K031/65 A61K031/56 A61K031/43.
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(hen or bird or chicken or turkey or egg or yolk).clm. and (pylori or pyloris or pylroi or pylorum or pyloridis or pyloris or helicobacter or hpylori or h-pylori).clm.	14

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<input type="checkbox"/>	L4	L3 and (porin or bab or bab-a or bab-b or baba1 or bab-a1 or hop or hopA or hopB or hopE or hopz or hop-z or hop-q)	6

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<input type="checkbox"/>	L1	bab-a or baba or (blood near5 adhesin) or (blood near5 adhesion) or (blood near15 pylori)	29107
<input type="checkbox"/>	L2	bab-a or baba or (blood near5 adhesin) or (blood near5 adhesion)	28832
<input type="checkbox"/>	L3	(11 or 12) and helicobact\$	402
<input type="checkbox"/>	L4	(11 or 12) same helicobact\$	191
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<input type="checkbox"/>	L6	15 same helicobact\$	9

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BAB A2
Bab b
Bab A
Omp 28
BabB/BabA1

20040234529. 22 Jan 04. 25 Nov 04. Helicobacter pylori adhesin binding group antigen. Boren, Thomas, et al. 424/164.1; 530/388.4 A61K039/40 C07K016/12.

☐ 2. 20040126811. 24 Dec 03. 01 Jul 04. Helicobacter pylori sialic acid binding adhesin, saba and saba-gene. Boren, Thomas, et al. 435/7.1; C12Q001/68 G01N033/53.

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☐ 8. 6410719. 10 Feb 98; 25 Jun 02. Blood group antigen binding protein and corresponding agents. Boren, Thomas, et al. 536/23.7; 536/23.1. C07H021/04.

☐ 9. WO009747646A1. 10 Jun 97. 18 Dec 97. HELICOBACTER PYLORI ADHESIN BINDING GROUP ANTIGEN. BOREN, THOMAS, et al. C07K014/205; A61K039/106 C07K016/12.

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Terms	Documents
L5 same helicobact\$	9

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**Adhesin binding fucosylated histo-
blood group antigen**

Synonyms	None
Gene name	Name: babA2
From	<i>Helicobacter pylori</i> (<i>Campylobacter pylori</i>) [TaxID: 210]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; <i>Helicobacter</i>

1/10 Z

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<input type="checkbox"/>	L1	anti-idioty\$ or antiidioty\$	3975
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<input type="checkbox"/>	L5	(anti-idioty\$ or antiidioty\$).ti,ab.clm. and (lewis\$ or fucos\$ or lea or leb or le-b).clm.	0

END OF SEARCH HISTORY

FEMS Immunol Med Microbiol. 1994 May;8(4):315-20.

[Related Articles, Links](#)

Isolation of an adhesin from *Staphylococcus aureus* that binds Lewis a blood group antigen and its relevance to sudden infant death syndrome.

Saadi AT, Weir DM, Poxton IR, Stewart J, Essery SD, Blackwell CC, Raza MW, Busuttill A.

Department of Medical Microbiology, University of Edinburgh, Medical School, UK.

A 67 kDa protein was isolated from cell membrane preparations of *Staphylococcus aureus* (NCTC 10655) by affinity adsorption with synthetic Lewis a antigen conjugated to Synsorb beads. Pre-treatment of buccal epithelial cells expressing Lewis a with the purified protein reduced binding of the staphylococcal strain to a greater extent than the material not bound to the Synsorb beads. The significance of this work is discussed with reference to expression of Lewis a antigen in infants and the proposed role of toxigenic strains of staphylococci in some cases of sudden infant death syndrome.

Trends Microbiol. 1994 Jul;2(7):221-8.

[Related Articles, Links](#)

Helicobacter pylori: molecular basis for host recognition and bacterial adherence.

Boren T, Normark S, Falk P.

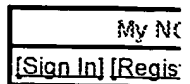
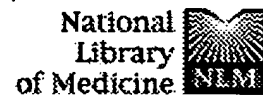
Dept of Molecular Microbiology, Washington University School of Medicine, St. Louis, MO 63110.

The bacterium *Helicobacter pylori* is tropic for epithelial cells and the mucus layer in the stomach lining, and is associated with the development of gastritis, ulcers and possibly also gastric malignancies. Adherence to the gastric epithelial cells is mediated by fucosylated blood-group antigens associated with blood-group O phenotype, which could explain the higher prevalence of ulcerative disease in individuals with this blood group.

Publication Types:

- Review
- Review, Tutorial

PMID: 8081648 [PubMed - indexed for MEDLINE]



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1: Adv Exp Med Biol. 1996;408:129-40.

Related Articles, Links

Interactions of bacterial adhesins with the extracellular matrix.

Ljungh A, Wadstrom T.

Department of Medical Microbiology, Lund University, Sweden.

Publication Types:

- Review
- Review, Tutorial

PMID: 8895785 [PubMed - indexed for MEDLINE]

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05292331 PMID: 351065

Studies on the question of conventional immunoglobulin on thymocytes from primitive vertebrates. II. Delineation between Ig-specific and cross-reactive membrane components.

Yamaga K M; Kubo R T; Etlinger H M
Journal of immunology (Baltimore, Md. - 1950) (UNITED STATES) Jun 1978,
120 (6) p2074-9, ISSN 0022-1767 Journal Code: 2985117R
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Subfile: AIM; INDEX MEDICUS
Tags: Female; Male; Research Support, U.S. Gov't, P.H.S.
Descriptors: *Antibody Specificity; *Cross Reactions; *Immunoglobulins;
*Salmonidae--immunology--IM; *T-Lymphocytes--immunology--IM; *Trout
--immunology--IM; Animals; Antibodies, Anti-Idiotypic; Fluorescent Antibody
Technique; **Fucose** --pharmacology--PD; Hemocyanin--immunology--IM; Immune
Sera--pharmacology--PD; Membrane Proteins--immunology--IM; Spleen
--immunology--IM
CAS Registry No.: 0 (Antibodies, Anti-Idiotypic); 0 (Immune Sera); 0
(Immunoglobulins); 0 (Membrane Proteins); 3713-31-3 (Fucose);
9013-72-3 (Hemocyanin)
Record Date Created: 19780828
Record Date Completed: 19780828

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00898266 JICST ACCESSION NUMBER: 89A0288646 FILE SEGMENT: JICST-E
**Analysis of Vh genes which encode the variable region of monoclonal
antibodies directed to cancer-associated carbohydrate antigens.**
KANNAGI REIJI (1); ZENITA KOICHI (1); HIRASHIMA KUNIMI (1); TAKADA AKIKO

(1)

(1) Kyoto Univ., Faculty of Medicine
Gan to Kagaku Ryoho(Japanese Journal of Cancer and Chemotherapy), 1989,
VOL.16,NO.3 Pt.2, PAGE.662-679, FIG.10, TBL.6, REF.30
JOURNAL NUMBER: Z0938AAH ISSN NO: 0385-0684
UNIVERSAL DECIMAL CLASSIFICATION: 616-006-09 577.1:576.8.097.5
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Review article
MEDIA TYPE: Printed Publication

ABSTRACT: Immune responses against cancer-associated, carbohydrate antigens are investigated by studying idiotypic determinants of specific antibodies with monoclonal anti-idiotypic antibodies, and by analyzing the structure of VH genes which encode the V region of the anti-carbohydrate antibodies. Four syngenic **antiidiotypic** antibodies towards monoclonal antibodies which are specific to the sialyl Lewis A antigen and two kinds of SSEA-1 related antigens (sialyl SSEA-1 and **fucosyl SSEA-1**) were obtained. Antibodies directed to carbohydrate antigens were mostly of IgM isotype, indicating these antigens are T-independent antigens, while anti-idiotypic monoclonal antibodies directed to those antibodies were mostly of IgG isotype, suggesting that T cells participate actively in the anti-idiotypic response. The Northern blotting analysis of VH genes of monoclonal antibodies directed to negatively-charged carbohydrate antigens such as gangliosides or sulfated glycolipids expressed the VH gene family J558 (group 1), followed by J606 (group 6) and Q52 (group 2) families. On the other hand, monoclonal antibodies directed to SSEA-1 related neutral carbohydrate antigens expressed VH genes of a minor family such as X24 (group 4), V31 (group 9), or 7183 (group 5). The same VH family as expressed in anti-SSEA-1 antibody (x24) was also expressed in the antibodies such as anti-I antibodies, which are directed to the synthetic precursors of the SSEA-1 antigen. In either case, the antibodies directed to one particular carbohydrate antigen tended to express the VH gene of one particular family exclusively. This suggests idiotypical homogeneity of the anti-carbohydrate antibodies.(author abst.)

DESCRIPTORS: tumor antigen; monoclonal antibody; idio type; tumor cell; immunotherapy; species specificity; epitope; CD15 antigen
BROADER DESCRIPTORS: antigen; antibody; idioblast; cell(cytology); therapy; biological comparison; comparison; differentiation antigen; surface antigen
CLASSIFICATION CODE(S): GE02030N; ED02030I
? t s2/3,kwic/3

2/3,KWIC/3 (Item 1 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.
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0124761 DBR Accession No.: 91-12403 PATENT
Gene encoding monoclonal antibody FH-2 variable region - glycochain antigen
SSEA-1, fucosyl SSEA-1, paragloboside FH-2, AH-6, 1B2 variable region
production; DNA sequence; anti-idiotype antibody production; cancer
screening, diagnosis
PATENT ASSIGNEE: Otsuka-Pharm. 1991
PATENT NUMBER: JP 3147788 PATENT DATE: 910624 WPI ACCESSION NO.:
91-227678 (9131)
PRIORITY APPLIC. NO.: JP 89285574 APPLIC. DATE: 891031
NATIONAL APPLIC. NO.: JP 89285574 APPLIC. DATE: 890131
LANGUAGE: Japanese

DESCRIPTORS: cancer-associated glycochain antigen SSEA-1, **fucosyl** SSEA-1,
paragloboside-specific monoclonal antibody FH-2, AH-6, 1B2 variable
region prep., gene...

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<input type="checkbox"/>	L6	lewis\$ near5 antigen\$	1044
<input type="checkbox"/>	L7	L6 and (antiidiot\$ or anti-idiot\$)	209
<input type="checkbox"/>	L8	L6 same (antiidiot\$ or anti-idiot\$)	18
<input type="checkbox"/>	L9	(lewis-b or lewisb or leb or le-b) near25 (antigen or blood or erythrocyte)	21

END OF SEARCH HISTORY

Spencer Notland

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Search for

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 744 AA (of which 7% low-complexity regions filtered out)

Date run: 2005-05-03 09:14:04 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,880,849 sequences; 604,459,357 total letters

UniProt Release 4.6 consists of: Swiss-Prot Release 46.6 of 26-Apr-2005: 180652 en
TrEMBL Release 29.6 of 26-Apr-2005: 1689375 entrie

[Taxonomic view](#)

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List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db AC	Description	Score	E-value
<input type="checkbox"/> tr Q9ZKV2	_HELPI Outer membrane protein-adhesin [babA] [Helicobac...	1382	0.0
<input type="checkbox"/> tr Q6T8D3	_HELPI BabA [Helicobacter pylori (Campylobacter pylori)]	1281	0.0
<input type="checkbox"/> tr Q7WV80	_HELPI Adhesin-binding fucosylated histo-blood group an...	1265	0.0
<input type="checkbox"/> tr Q7WV81	_HELPI Adhesin-binding fucosylated histo-blood group an...	1262	0.0
<input type="checkbox"/> tr Q25840	_HELPI Outer membrane protein (Omp28) [HP1243] [Helicob...	1258	0.0
<input type="checkbox"/> tr Q7WV79	_HELPI Adhesin-binding fucosylated histo-blood group an...	1252	0.0
<input type="checkbox"/> tr Q52269	_HELPI Adhesin binding fucosylated histo-blood group an...	1242	0.0
<input type="checkbox"/> tr Q7WV84	_HELPI Adhesin-binding fucosylated histo-blood group an...	1241	0.0
<input type="checkbox"/> tr Q5Q1P2	_HELPI BabB/BabA1 fusion protein 1 (Fragment) [babB/bab...	1217	0.0
<input type="checkbox"/> tr Q6JAA0	_HELPI Adhesin-binding fucosylated histo-blood group an...	1215	0.0


<input type="checkbox"/>	tr	Q7WV83	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1214	0.0
<input type="checkbox"/>	tr	Q7WV78	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1212	0.0
<input type="checkbox"/>	tr	Q7WV75	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1212	0.0
<input type="checkbox"/>	tr	Q5Q1P1	_HELPHY	BabB/BabA1 fusion protein 2 (Fragment) [babB/bab...	1212	0.0
<input type="checkbox"/>	tr	Q7WV76	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1212	0.0
<input type="checkbox"/>	tr	Q6JA97	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1212	0.0
<input type="checkbox"/>	tr	Q7WV74	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1207	0.0
<input type="checkbox"/>	tr	Q6JA99	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1206	0.0
<input type="checkbox"/>	tr	Q7WV73	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1198	0.0
<input type="checkbox"/>	tr	Q7WV77	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1197	0.0
<input type="checkbox"/>	tr	Q9R7I4	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1196	0.0
<input type="checkbox"/>	tr	Q7WV72	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1196	0.0
<input type="checkbox"/>	tr	Q6JA98	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1193	0.0
<input type="checkbox"/>	tr	Q7WV85	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1191	0.0
<input type="checkbox"/>	tr	Q7WV68	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1185	0.0
<input type="checkbox"/>	tr	Q7WV69	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1185	0.0
<input type="checkbox"/>	tr	Q7WV67	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1184	0.0
<input type="checkbox"/>	tr	Q7WV71	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1183	0.0
<input type="checkbox"/>	tr	Q6JAA1	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1182	0.0
<input type="checkbox"/>	tr	Q7WV82	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1171	0.0
<input type="checkbox"/>	tr	Q7WV66	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1160	0.0
<input type="checkbox"/>	tr	Q7WV70	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	1157	0.0
<input type="checkbox"/>	tr	Q25086	_HELPHY	Outer membrane protein (Omp9) [HP0317] [Helicoba...	917	0.0
<input type="checkbox"/>	tr	O51811	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	875	0.0
<input type="checkbox"/>	tr	Q7WVA2	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	868	0.0
<input type="checkbox"/>	tr	Q7WVA4	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	864	0.0
<input type="checkbox"/>	tr	Q9ZJY3	_HELPHJ	Outer membrane protein-adhesin [babB] [Helicobac...	862	0.0
<input type="checkbox"/>	tr	Q6T8D5	_HELPHY	BabB (BabB2) [Helicobacter pylori (Campylobacter...	860	0.0
<input type="checkbox"/>	tr	Q25556	_HELPHY	Outer membrane protein (Omp19) [HP0896] [Helicob...	860	0.0
<input type="checkbox"/>	tr	Q7WVA1	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	857	0.0
<input type="checkbox"/>	tr	Q7WVA0	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	845	0.0
<input type="checkbox"/>	tr	Q7WVA3	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	844	0.0
<input type="checkbox"/>	tr	Q7WV97	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	844	0.0
<input type="checkbox"/>	tr	Q7WVA5	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	839	0.0
<input type="checkbox"/>	tr	Q7WV95	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	839	0.0
<input type="checkbox"/>	tr	Q7WV99	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	838	0.0
<input type="checkbox"/>	tr	Q7WV98	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	838	0.0
<input type="checkbox"/>	tr	Q7WV93	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	835	0.0
<input type="checkbox"/>	tr	Q7WV94	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	831	0.0
<input type="checkbox"/>	tr	Q7WV88	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	829	0.0
<input type="checkbox"/>	tr	Q7WV96	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	827	0.0
<input type="checkbox"/>	tr	Q7WV86	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	823	0.0
<input type="checkbox"/>	tr	Q7WV92	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	821	0.0
<input type="checkbox"/>	tr	Q7WV89	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	818	0.0
<input type="checkbox"/>	tr	Q7WV90	_HELPHY	Adhesin-binding fucosylated histo-blood group an...	817	0.0

<input type="checkbox"/>	tr Q7WV91	_HELPE Adhesin-binding fucosylated histo-blood group an...	814	0.0
<input type="checkbox"/>	tr Q7WV87	_HELPE Adhesin-binding fucosylated histo-blood group an...	813	0.0
<input type="checkbox"/>	tr Q9X746	_HELPE HopZ protein precursor [hopZ] [Helicobacter pylo...	694	0.0
<input type="checkbox"/>	tr Q9X748	_HELPE HopZ protein precursor [hopZ] [Helicobacter pylo...	690	0.0
<input type="checkbox"/>	tr Q9S3I7	_HELPE HopZ protein precursor [hopZ] [Helicobacter pylo...	690	0.0
<input type="checkbox"/>	tr Q9ZN51	_HELPE Putative Outer membrane protein [JHP0007] [Helic...	689	0.0
<input type="checkbox"/>	tr Q9X747	_HELPE HopZ protein precursor [hopZ] [Helicobacter pylo...	687	0.0
<input type="checkbox"/>	tr Q9X745	_HELPE HopZ protein precursor [hopZ] [Helicobacter pylo...	683	0.0
<input type="checkbox"/>	tr Q9ZN38	_HELPE Putative Outer membrane protein [JHP0021] [Helic...	681	0.0
<input type="checkbox"/>	tr Q24870	_HELPE Outer membrane protein (Omp2) [HP0025] [Helicoba...	673	0.0
<input type="checkbox"/>	tr Q34523	_HELPE Outer membrane protein (Omp29) (Omp5) [HP0227] [...]	636	0.0
<input type="checkbox"/>	tr Q9Z390	_HELPE Putative Outer membrane protein [JHP0212] [Helic...	622	e-176
<input type="checkbox"/>	tr Q8GDI6	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	545	e-153
<input type="checkbox"/>	tr Q8GDJ1	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	545	e-153
<input type="checkbox"/>	tr Q8GDI7	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	545	e-153
<input type="checkbox"/>	tr Q8GDI8	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	540	e-152
<input type="checkbox"/>	tr Q8GDJ2	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	537	e-151
<input type="checkbox"/>	tr Q8GDJ3	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	532	e-150
<input type="checkbox"/>	tr Q8GDJ4	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	526	e-148
<input type="checkbox"/>	tr Q9ZK39	_HELPE Putative Outer membrane function [JHP1103] [Heli...	512	e-143
<input type="checkbox"/>	tr Q8GDI9	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	506	e-142
<input type="checkbox"/>	tr Q25791	_HELPE Outer membrane protein (Omp27) [HP1177] [Helicob...	496	e-138
<input type="checkbox"/>	tr Q8GDJ0	_HELPE HopQ [hopQ] [Helicobacter pylori (Campylobacter ...]	495	e-138
<input type="checkbox"/>	tr Q6DSZ4	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	445	e-123
<input type="checkbox"/>	tr Q6DSZ1	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	437	e-121
<input type="checkbox"/>	tr Q6DSY5	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	429	e-118
<input type="checkbox"/>	tr Q6DSZ8	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	427	e-118
<input type="checkbox"/>	tr Q6DSX1	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	422	e-116
<input type="checkbox"/>	tr Q6DSZ6	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	419	e-116
<input type="checkbox"/>	tr Q6DSY9	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	418	e-115
<input type="checkbox"/>	tr Q6DSY0	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	416	e-115
<input type="checkbox"/>	tr Q6DSY7	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	415	e-114
<input type="checkbox"/>	tr Q6DSY6	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	412	e-113
<input type="checkbox"/>	tr Q6DT16	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	404	e-111
<input type="checkbox"/>	tr Q6DSX0	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	404	e-111
<input type="checkbox"/>	tr Q6DT06	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	402	e-110
<input type="checkbox"/>	tr Q6DT01	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	400	e-110
<input type="checkbox"/>	tr Q6DSZ0	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	398	e-109
<input type="checkbox"/>	tr Q6DSZ9	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	396	e-108
<input type="checkbox"/>	tr Q6DSZ7	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	393	e-108
<input type="checkbox"/>	tr Q6DSZ3	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	390	e-107
<input type="checkbox"/>	tr Q6DT04	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	389	e-106
<input type="checkbox"/>	tr Q6DSX3	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	388	e-106
<input type="checkbox"/>	tr Q6DSZ2	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	387	e-106
<input type="checkbox"/>	tr Q6DSW8	_HELPE Adhesin (Fragment) [babA] [Helicobacter pylori (...]	387	e-106

Graphical overview of the alignments

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to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits

Pfam hits

HP_OMP

Submission	Matches on query sequence		Mat
	1	500	
Q9ZKV2			
Q6T8D3			
Q7MV80			
Q7MV81			
Q25840			
Q7MV79			
Q52269			
Q7MV84			
Q5Q1P2			
Q6JAA0			
Q7MV83			
Q7MV78			
Q7MV75			
Q5Q1P1			
Q7MV76			
Q6JAA7			
Q7MV74			
Q6JAA9			
Q7MV73			
Q7MV77			
Q9R7I4			
Q7MV72			
Q6JAA8			
Q7MV85			
Q7MV68			
Q7MV69			
Q7MV67			
Q7MV71			
Q6JAA1			
Q7MV82			
Q7MV66			
Q7MV70			
Q25086			
Q51811			
Q7MVA2			
Q7MVA4			
Q9ZJY3			
Q6T8D5			
Q25556			
Q7MVA1			
Q7MVA0			
Q7MVA3			
Q7MV97			
Q7MVA5			
Q7MV95			
Q7MV99			
Q7MV98			
Q7MV93			
Q7MV94			
Q7MV88			
Q7MV96			
Q7MV86			
Q7MV92			
Q7MV89			
Q7MV90			
Q7MV91			
Q7MV87			
Q9X746			
Q9X748			
Q9S3I7			
Q9ZN51			
Q9X747			
Q9X745			
Q9ZN38			
Q24870			
Q34523			
Q9Z390			
Q8GDI6			
Q8GDJ1			
Q8GDI7			
Q8GDI8			
Q8GDJ2			
Q8GDJ3			
Q8GDJ4			
Q9ZK39			
Q8GDI9			
Q25791			
Q8GDJ0			
Q6DSZ4			
Q6DSZ1			
Q6DSY5			
Q6DSZ8			
Q6DSX1			
Q6DSZ6			
Q6DSY9			
Q6DSY0			

Alignments

tr Q9ZKV2 Outer membrane protein-adhesin [babA] [Helicobacter 744
Q9ZKV2_HELPJ pylori J99 AA
(Campylobacter pylori J99)] align

Score = 1382 bits (3577), Expect = 0.0
Identities = 692/744 (93%), Positives = 692/744 (93%)

Query: 1 MKKHIXXXXXXXXXXXXXAEDDGFYTSVGYQIGEEAQMVTNTKGIQDLSDRYESLNNLL 60
MKKHI AEDDGFYTSVGYQIGEEAQMVTNTKGIQDLSDRYESLNNLL
Sbjct: 1 MKKHILSLTEGSLLVSTLSAEDDGFYTSVGYQIGEEAQMVTNTKGIQDLSDRYESLNNLL 60

Query: 61 NRYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANSPAYQAVLLAINAAVGFWNVV 120
NRYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANSPAYQAVLLAINAAVGFWNVV
Sbjct: 61 NRYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANSPAYQAVLLAINAAVGFWNVV 120

Query: 121 GYVTQCGGNANGQKSISSTKIFNNEPGYRSTSITCSLNGHSPGYYGPMSENFKKLNEAY 180
GYVTQCGGNANGQKSISSTKIFNNEPGYRSTSITCSLNGHSPGYYGPMSENFKKLNEAY
Sbjct: 121 GYVTQCGGNANGQKSISSTKIFNNEPGYRSTSITCSLNGHSPGYYGPMSENFKKLNEAY 180

Query: 181 QILQTALKRGLPALKENNGKVNVTYTYTCSGDGNNNCSSQVTGVNNQKDGTCTKIQTIDG 240
QILQTALKRGLPALKENNGKVNVTYTYTCSGDGNNNCSSQVTGVNNQKDGTCTKIQTIDG
Sbjct: 181 QILQTALKRGLPALKENNGKVNVTYTYTCSGDGNNNCSSQVTGVNNQKDGTCTKIQTIDG 240

Query: 241 KSVTTTISSKVVDSRADGNTTGVSYTEITNKLEGVPDXXXXXXXXXXTLINTINNACPYF 300
KSVTTTISSKVVDSRADGNTTGVSYTEITNKLEGVPD TLINTINNACPYF
Sbjct: 241 KSVTTTISSKVVDSRADGNTTGVSYTEITNKLEGVPDSAQALLAQASTLINTINNACPYF 300

Query: 301 HASNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQTTPVGNN 360
HASNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQTTPVGNN
Sbjct: 301 HASNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQTTPVGNN 360

Query: 361 NGKPFNPFTDASFAQGMLANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFLATCNN 420
NGKPFNPFTDASFAQGMLANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFLATCNN
Sbjct: 361 NGKPFNPFTDASFAQGMLANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFLATCNN 420

Query: 421 XXXXXXXXXXXXXXXVTTQTTFASGCAYVQGTITNLKNSIAHFGTXXXXXXXXXXXXDTL 480
VTTQTTFASGCAYVQGTITNLKNSIAHFGT DTL
Sbjct: 421 PSTAGTGGTQGSAPGTVTTQTTFASGCAYVQGTITNLKNSIAHFGTQEQQIQQAENIADTL 480

Query: 481 VNFKSRYSSELGNTYNSITTALSNI PNAQSLQNAVSKKNNPYS PQGIDTNYLLNQNSYNQI 540
VNFKSRYSSELGNTYNSITTALSNI PNAQSLQNAVSKKNNPYS PQGIDTNYLLNQNSYNQI
Sbjct: 481 VNFKSRYSSELGNTYNSITTALSNI PNAQSLQNAVSKKNNPYS PQGIDTNYLLNQNSYNQI 540

Query: 541 QTINQELGRNPFRKVGIVSSQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAF 600
QTINQELGRNPFRKVGIVSSQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAF
Sbjct: 541 QTINQELGRNPFRKVGIVSSQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAF 600

Query: 601 IKSSFFNSASDVWVTYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY 660
IKSSFFNSASDVWVTYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY
Sbjct: 601 IKSSFFNSASDVWVTYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY 660

Query: 661 VNLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNY 720
VNLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNY
Sbjct: 661 VNLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNY 720

Query: 721 YSFMGAELKYRRLYSVYLNIVFAY 744
 YSFMGAELKYRRLYSVYLNIVFAY
 Sbjct: 721 YSFMGAELKYRRLYSVYLNIVFAY 744

tr Q6T8D3 BabA [Helicobacter pylori (Campylobacter 742 AA
 Q6T8D3_HELPY pylori)] align

Score = 1281 bits (3314), Expect = 0.0

Identities = 639/726 (88%), Positives = 657/726 (90%), Gaps = 1/726 (0%)

Query: 20 AEDDGFYTSVGYQIGEEAQMVTNTKGIQDLSDRYESLNNLLNRYSTLNTLIKLSADPSAI 79
 AEDDGFYTSVGYQIGEEAQMVTNTKGIQ LSD YE LNNLL RYSTLNTLIKLSADPSAI
 Sbjct: 17 AEDDGFYTSVGYQIGEEAQMVTNTKGIQQLSDNYEKLNNLLTRYSTLNTLIKLSADPSAI 76

Query: 80 NAVRENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNVVGYVTQCGGNANGQKSISSK 139
 NAVRENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNVVGYVTQCGGN NGQ+S SS
 Sbjct: 77 NAVRENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNVVGYVTQCGGNMNGQESTSST 136

Query: 140 TIFNNEPGYRSTSITCSLNGHSPGYGPMSENFKKLNEAYQILQTALKRGLPALKENNG 199
 TIFNNEPG+RS SITCSLNG+ PGYGPMSENFKKLNEAYQILQTALK+GLPALKENNG
 Sbjct: 137 TIFNNEPGHRSASITCSLNGYKPGYGPMSENFKKLNEAYQILQTALKQGLPALKENNG 196

Query: 200 KVN-VTTYTYTCSGDGNNNCSSQVTGVNNQKDGTCTKIQTIDGKSVTTTISSKVVDSDRADG 258
 + VTTYTYTCSG GNNNC3 Q TG+N Q G+KT IQTIDGK+V TTIS KVVDS A G
 Sbjct: 197 TLKEVTTYTYTCSGKGNNNCSEQATGINRQNGGSKTTIQTIDGKTVRTTISLKVVDSTASG 256

Query: 259 NTTGVSYTEITNKLEGPDXXXXXXXXXXXTLINTINNACPYFHASNSSEANAPKFSTTTG 318
 NT+ VSYTEITNKL+GVPD TLINTIN ACPYFHA+NSSEANAPKFSTT+G
 Sbjct: 257 NTSHVSYTEITNKLDGVPDQAQALLAQASTLINTINEACPYFHANNSSSEANAPKFSTTSG 316

Query: 319 KICGAFSEEEISAIQKMITDAQELVNQTSVINEHEQTTPVGNNGKPFNPFTDASFAQGML 378
 KICGAFSEEEISAIQKMITDAQELVNQTSVINEHEQ+TP+GNNGKPFNP+TDASFAQGML
 Sbjct: 317 KICGAFSEEEISAIQKMITDAQELVNQTSVINEHEQSTPIGNNGKPFNPYTDASFAQGML 376

Query: 379 ANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFLATCENNXXXXXXXXXXXXXXXXXVT 438
 ANA AQAQKMLNLAEQVGQAINPERLSG F+NEV GFLATCEN VT
 Sbjct: 377 ANAQAQKMLNLAEQVGQAINPERLSGAFKNFVTGFLATCENNPSTAGTSGTQGSAPGTVT 436

Query: 439 TQTFASGCAYVGQTITNLKNSIAHFGTXXXXXXXXXXXXDLVNFKSRYSELGNTYNSIT 498
 TQTFASGCAYV QTITNL NSI HFGT DTLVNFKSRYSELGNTYNSIT
 Sbjct: 437 TQTFASGCAYVEQTITNLNTSITHFGTQEQQIQQAENIADTLVNFKSRYSELGNTYNSIT 496

Query: 499 TALSNI PNAQSLQNAVSKKNPYPSPQIDTNYLLNQNSYNQIQ TINQELGRNPFRKVGIV 558
 TALS+IPNAQSLQNAVSKKNPYPSPQGI+TNYYLNQNSYNQIQ TINQELGRNPFRKVGIV
 Sbjct: 497 TALSSIPNAQSLQNAVSKKNPYPSPQGIETNYLLNQNSYNQIQ TINQELGRNPFRKVGIV 556

Query: 559 SSQTNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAFIKSSFFNSASDVWTYGFG 618
 SSQTNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAFIKSSFFNSASDVWTYGFG
 Sbjct: 557 SSQTNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAFIKSSFFNSASDVWTYGFG 616

Query: 619 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEYVNLATMNNVYNAMNVAN 678
 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEYVNLATMNNVYNAMNVAN
 Sbjct: 617 ADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEYVNLATMNNVYNAMNVAN 676

Query: 679 FQFLFNMGVRMNLARPKKKDSHAAQHGIELGLKIPTINTNYYSFMGAELKYRRLYSVYL 738

FQFLNMGVMMNLARPKKKSDHAAQHGIELGLKIPTINTNYYSFMGAELKYRRLYSVYL
 Sbjct: 677 FQFLNMGVMMNLARPKKKSDHAAQHGIELGLKIPTINTNYYSFMGAELKYRRLYSVYL 736
 Query: 739 NYVFAY 744
 NYVFAY
 Sbjct: 737 NYVFAY 742

tr Q7WV80 Adhesin-binding fucosylated histo-blood group antigen 736
 Q7WV80_HELPY (Fragment) AA
 [babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 1265 bits (3274), Expect = 0.0
 Identities = 633/737 (85%), Positives = 654/737 (87%), Gaps = 1/737 (0%)

Query: 1 MKKHIXXXXXXXXXXXXXAEDDGFYTSVGYQIGEAQMVTNTKGIQDLSDRYESLNNLL 60
 MKKHI AEDDGFY S GYQIGEAQMVTNTKGIQ LSD YE+LNNLL
 Sbjct: 1 MKKHILSLTLGSLLVSTLSAEDDGFYMSAGYQIGEAQMVTNTKGIQQLSDNYENLNNLL 60
 Query: 61 NRYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANSPAYQAVLLAINAAVGFWNVV 120
 RYSTLNTLIKLSADPSAINA RENLGASAKNLIGDKANSPAYQAVLLAINAAVGFWNVV
 Sbjct: 61 TRYSTLNTLIKLSADPSAINAARENLGASAKNLIGDKANSPAYQAVLLAINAAVGFWNVV 120
 Query: 121 GYVTQCGGNANGQKSISSKTIFNNEPGYRSTSITCSLNGHSPGYGPMSENFKKLNEAY 180
 GYVTQCGGNANGQ+S SS TIFNNEPGYRSTSITCSLN + PGYGPMSENFKKLNEAY
 Sbjct: 121 GYVTQCGGNANGQESTSSTTIFNNEPGYRSTSITCSLNRYVPGYGPMSENFKKLNEAY 180
 Query: 181 QILQTALKRGLPALKENNGKVNVTYTYTCSGDGNNNCSSQVTGVNNQKDGTCTKIQTIDG 240
 QILQTALK GLPALKENNGKV+V+YTYTCSG+GNNNC + TGV Q +KT+ Q IDG
 Sbjct: 181 QILQTALKNGLPALKENNGKVDVSYTYTCSGEGNNNCSEATGVE-QNGRSKTETQIIDG 239
 Query: 241 KSVTTTISSEKVVDSRADGNTTGVSYTEITNKLEGPDPDXXXXXXXXXXTLINTINNACPYF 300
 KSVTTTISSEKVVDS+A GNT+GVSYTEITNKL+GVED TLINTIN ACPYF
 Sbjct: 240 KSVTTTISSEKVVDSKAAGNTSGVSYTEITNKLDGVPDQAQALLAQASTLINTINNACPYF 299
 Query: 301 HASNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQTTPVGNN 360
 A+NSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQ+TP+GNN
 Sbjct: 300 RANNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQSTPIGNN 359
 Query: 361 NGKPFNPFTDASFAQGMLANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFILATCNN 420
 NGKPFNPFTDASFAQGMLANASQAQKMLNLA QVGQ INP+ L+G F+NEV GFILATCNN
 Sbjct: 360 NGKPFNPFTDASFAQGMLANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFILATCNN 419
 Query: 421 XXXXXXXXXXXXXXXVTTQTFAAGCAYVGTITNLKNSIAHFGTXXXXXXXXXXXXDTL 480
 VTTQTFAAGCAYV QTITNL NSIAHFGT DTL
 Sbjct: 420 PSTAGTGGTQGSAPGTVTTQTFAAGCAYVEQTITNLNSIAHFGTQEQQIQQAENIADTL 479
 Query: 481 VNFKSRYSELGNTYNSITTALSNIIPNAQSLQNAVSKKNPYSPQIDTNYLLNQNSYNQI 540
 VNFKSRY+ELGNTYNSITTALSNIIPNAQSLQNAVSKKNPYSPQGI+TNYLLNQNSYNQI
 Sbjct: 480 VNFKSRYNELGNTYNSITTALSNIIPNAQSLQNAVSKKNPYSPQGIETNYLLNQNSYNQI 539
 Query: 541 QTINQELGRNPFRKVGIVSSQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAF 600
 QTINQELGRNPFRKVGIV SQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAF
 Sbjct: 540 QTINQELGRNPFRKVGIVSGQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAF 599
 Query: 601 IKSSFFNSASDVWTYGFGADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY 660

```

      IKSSFFNSASDVWTFYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY
Sbjct: 600 IKSSFFNSASDVWTFYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY 659

      VNLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKDSHAAQHGIELGLKIPTINTNY 720
      VNLAT+NNVYNAKMNVANFQFLFNMGVRMNLARPKKKDSHAAQHGIELGLKIPTINTNY
Sbjct: 660 VNLATVNNVYNAKMNVANFQFLFNMGVRMNLARPKKKDSHAAQHGIELGLKIPTINTNY 719

      YSFMGAELKYRRLYSVY 737
      YSFMGAELKYRRLYSVY
Sbjct: 720 YSFMGAELKYRRLYSVY 736

```

```

tr Q7WV81      Adhesin-binding fucosylated histo-blood group antigen      737
  Q7WV81_HELPY (Fragment)      AA
                [babB] [Helicobacter pylori (Campylobacter pylori)]      align

```

Score = 1262 bits (3266), Expect = 0.0
 Identities = 632/737 (85%), Positives = 651/737 (87%)

```

Query: 1  MKKHIXXXXXXXXXXXXXAEDDGFYTSVGYQIGEAQMVTNTKGIQDLSDRYESLNNLL 60
      MKKHI      AEDDGFYTSVGYQIGEAQMVTNTKGIQDLSDRYESLNNLL
Sbjct: 1  MKKHILSLTLGSLLVSTLSAEDDGFYTSVGYQIGEAQMVTNTKGIQDLSDRYESLNNLL 60

Query: 61  NRYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNV 120
      NRYSTLNTLIKLSADPSAINA RENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNV
Sbjct: 61  NRYSTLNTLIKLSADPSAINAARENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNV 120

Query: 121 GYVTQCGGNANGQKSISSTIFNNEPGYRSTSITCSLNGHSPGYGPMSENFKKLNEAY 180
      GYVTQCGGNA+G++S SS TIFNNEPGYRSTSITCSLNGH SPGYGPMSENFKKLNEAY
Sbjct: 121 GYVTQCGGNAHGRESTSSTTIFNNEPGYRSTSITCSLNGHRPGYGPMSENFKKLNEAY 180

Query: 181 QILQTALKRGLPALKENNGKVNVTYTYTCSGDGNNNCSSQVTGVNNQKDGTCTKIQTIDG 240
      QILQTALK+GLEALKENN VNVTYTYTCSGDGN+NCS VTCVN+Q +GTRT QTIDG
Sbjct: 181 QILQTALKQGLPALKENNRTVNVTYTYTCSGDGNDNCS PNVTVNDQHNGTKTTTQTIDG 240

Query: 241 KSVTTTISSKVVDSDRADGNTTGVSYTEITNKLEGVPDXXXXXXXXXXTLINTINNACPYF 300
      KSVTTTISSKVVDSD A NT+ VSYTEITN L VPD      TLINTIN AGP+F
Sbjct: 241 KSVTTTISSKVVDSDNAKDNTSHVSYTEITNHLNDVPDQAALLAQASTLINTINTACPF 300

Query: 301 HASNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQTTPVGNN 360
      HA+NSSEANAPKFSTT GKICGAFSEEIS IQKMITDAQELVNQTSVIN +EQ+TPV N
Sbjct: 301 HANNSSSEANAPKFSTTIGKICGAFSEEISTIQKMITDAQELVNQTSVINSNEQSTPVDGN 360

Query: 361 NGKPFNPFTDASFAQGMLANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFLATCNN 420
      NGKPFNPFTDASEAQGMLANASQAQKMLNLA QVGQAINPE L+G+F+NFV GELATCNN
Sbjct: 361 NGKPFNPFTDASFAQGMLANASQAQKMLNLAHQVGQAINPENLTGSFKNFVTGFLATCNN 420

Query: 421 XXXXXXXXXXXXXXXXVTTQTTFASGCAYVQTITNLKNSIAHFGTXXXXXXXXXXXXDTL 480
      VTTQTTFASGCAYV QTITNL NSIAHFGT      DTL
Sbjct: 421 LSTAGTGSTQGSAPGTVTTQTTFASGCAYVEQTITNLNSIAHFGTQEQQIQQAENIADTL 480

Query: 481 VNFKSRYSSELGNTYNSITTALSNIPNAQSLQNAVSKKNNPYPSPQGIDTNYLLNQNSYNQI 540
      VNF+SRYSSELGNTYNSITTALS +PNAQSLQN VSKKNNPYPSPQGIDTNYLLNQNSYNQI
Sbjct: 481 VNFRRYSSELGNTYNSITTALSKVPNAQSLQNVVSKKNNPYPSPQGIDTNYLLNQNSYNQI 540

Query: 541 QTINQELGRNPFRKVGIVSSQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAF 600

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          QTINQELGRNPFPRKVGIV SQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFEDYNHAF
Sbjct: 541 QTINQELGRNPFPRKVGIVGSQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFEDYNHAF 600

Query: 601 IKSSFFNSASDVWTYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY 660
          IKSSFFNSASDVWTYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY
Sbjct: 601 IKSSFFNSASDVWTYGFADALYNFINDKATNFLGKNNKLSVGLFGGIALAGTSWLNSEY 660

Query: 661 VNLATMNNVYNAKMNVANFQFLFNMGVRMNLARPKKKSDHAAQHGIELGLKIPTINTNY 720
          VNLATMNNVYNAKMNVANFQFLFNMGVRMNLAR KKK SDHAAQHGIELG+KIPTINTNY
Sbjct: 661 VNLATMNNVYNAKMNVANFQFLFNMGVRMNLARSKKKSDHAAQHGIELGVKIPTINTNY 720

Query: 721 YSFMGAELKYRRLYSVY 737
          YSFMGAELKYRRLYSVY
Sbjct: 721 YSFMGAELKYRRLYSVY 737

```

```

tr O25840      Outer membrane protein (Omp28) [HP1243] [Helicobacter      733
    O25840_HELPY pylori
                  (Campylobacter pylori)]
                                     AA
                                     align

```

Score = 1258 bits (3255), Expect = 0.0
 Identities = 636/744 (85%), Positives = 652/744 (87%), Gaps = 11/744 (1%)

```

Query: 1  MKKHIXXXXXXXXXXXXXXXXXAEDDGFYTSVGYQIGEEAQMVTNTKGIQDLSDRYESLNNLL 60
          MKKHI AEDDGFYTSVGYQIGEEAQMVTNTKGIQ LSD YE+IANNLL
Sbjct: 1  MKKHILSLALGSLVSTLSAEDDGFYTSVGYQIGEEAQMVTNTKGIQQLSDNYENLNNLL 60

Query: 61  NRYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNVV 120
          RYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNVV
Sbjct: 61  TRYSTLNTLIKLSADPSAINAVRENLGASAKNLIGDKANS PAYQAVLLAINAAVGFWNVV 120

Query: 121 GYVTQCGGNANGQKSISSTKTFNNEPGYRSTSITCSLNGHSPGYGPMSENFKKLNEAY 180
          GYVTQCGGNANGQ+S SS TTFNNEPGYRSTSITCSLNGH PGYGPMSENFKKLNEAY
Sbjct: 121 GYVTQCGGNANGQESTSSTTFNNEPGYRSTSITCSLNGHKPGYGPMSENFKKLNEAY 180

Query: 181 QILQTALKRGLPALKENNGKVNVTYTYTCSGDNMNCSSQVTGVNNQKDGTCTKIQTIDG 240
          QILQTALK GLPALKENNGKV+VPTYTYTCSG GNNCS V +GTKT QTIDG
Sbjct: 181 QILQTALKNGLPALKENNGKVSVTYTYTCSGQGNMNCSPSV-----NGTKTTTQTIDG 233

Query: 241 KSVTTTISSKVVDSRADGNTTGVSYTEITNKLEGVPDXXXXXXXXXXTLINTINNACPYF 300
          KSVTTTISSKVV S A GNT+ V ITNKL+GVPD TLINTIN ACPYF
Sbjct: 234 KSVTTTISSKVVGSIASGNTSHV----ITNKLDGVPDSAQALLAQASTLINTINEACPYF 289

Query: 301 HASNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINEHEQTTPVGNN 360
          HA+NSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVIN +EQ+TFVGNN
Sbjct: 290 HATNSSEANAPKFSTTTGKICGAFSEEISAIQKMITDAQELVNQTSVINSNEQSTPVGNN 349

Query: 361 NGKPFNPFTDASFAQGMLANASQAQKMLNLAEQVGQAINPERLSGTFQNFVKGFLATCNN 420
          NGKPFNPFTDASFAQGMLANASQAQKMLNLA QVGQAINPE LS F+NEV GFLATCNN
Sbjct: 350 NGKPFNPFTDASFAQGMLANASQAQKMLNLAHQVGQAINPENLSENFKNFVTGFLATCNN 409

Query: 421 XXXXXXXXXXXXXXXXXXXVTTQTFAAGCAYVQTITNLKNSIAHFGTXXXXXXXXXXXXDTL 480
          VTTQTFAAGCAYV QT+TNL NSIAHFGT DTL
Sbjct: 410 KSTAGTGGTQGSAPGTVTTQTFAAGCAYVEQTLNLGNSIAHFGTQEQQIQQAENIADTL 469

Query: 481 VNFKSRYSELGNTYNSITTALSNIPNAQSLQNAVSKKNNPYSPOGIDTNYILNQNSYNQI 540

```

2826561 PMID: 10762234

Functional expression in Escherichia coli and membrane topology of porin HopE, a member of a large family of conserved proteins in Helicobacter pylori.

Bina J; Bains M; Hancock R E

Department of Microbiology, University of British Columbia, Vancouver, British Columbia V6T 1Z3, Canada.

Journal of bacteriology (UNITED STATES) May 2000, 182 (9) p2370-5, ISSN 0021-9193 Journal Code: 2985120R

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HopE is one of the smallest members of a family of 31 outer membrane proteins in *Helicobacter pylori* and has been shown to function as a **porin**. In this study it was cloned into *Escherichia coli* where it was expressed in the outer membrane, as confirmed by indirect immunofluorescence using HopE-specific antibodies. HopE purified from *E. coli* reconstituted channels in planar bilayer membranes that were the same size as those formed by HopE purified from *H. pylori*. A model of the membrane topology of HopE was constructed and indicated that this protein formed a beta-barrel with 16 transmembrane amphipathic beta-strands. The accuracy of this model was tested by linker insertion mutagenesis, assuming that, like other **porins**, amino acid insertions were not tolerated in the transmembrane beta-strands but were tolerated in the adjoining loop regions. Generally, the results obtained with a series of 12 insertions of the sequence RSKDV and two substitutions were consistent with the topological model. The preponderance of amino acids that were **conserved** in the extended family of HopE paralogs were predicted to be within the membrane and comprised 45% of all residues in the membrane.

Tags: Research Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--metabolism--ME; *Escherichia coli--metabolism--ME; *Helicobacter pylori--metabolism--ME; *Porins--metabolism--ME; Amino Acid Sequence; Cloning, Molecular; Gene Expression; Helicobacter pylori--genetics--GE; Models, Biological; Molecular Sequence Data; Porins--genetics--GE

CAS Registry No.: 0 (Bacterial Proteins); 0 (Porins)

Record Date Created: 20000613

Record Date Completed: 20000613

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05may05 12:44:23 User228206 Session D2441.6

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\$0.21 1 Type(s) in Format 9

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\$0.30 Estimated cost File155

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 OneSearch, 9 files, 0.258 DialUnits FileOS
\$0.26 TELNET
\$2.04 Estimated cost this search
\$2.04 Estimated total session cost 0.258 DialUnits

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